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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 9.33333 Seconds
(without alignments)
154.634 Million cell updates/sec

Title: US-09-423-351C-9

Perfect score: 76

Sequence: 1 DEAQSKRGILTLKYP 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	76	100.0	86	2 C43616	actin beta, cytosolic
2	76	100.0	137	2 A28258	actin 5C - fruit fly
3	76	100.0	158	2 I49465	alpha-cardiac actin
4	76	100.0	195	2 S20097	actin 85c - potato
5	76	100.0	213	2 A61043	actin CAL5 - sea slug
6	76	100.0	308	2 A03000	actin 3 - fruit fly
7	76	100.0	325	2 J20008	actin homolog prot
8	76	100.0	327	2 S11452	actin (clone 302)
9	76	100.0	328	2 S05430	actin beta - grass
10	76	100.0	349	2 B25819	actin, fetal skeletal
11	76	100.0	361	2 S68089	actin 2 - Arabidopsis
12	76	100.0	362	2 A26559	actin type 5, cyto
13	76	100.0	362	2 S68090	actin 8 - Arabidopsis
14	76	100.0	365	2 A37431	actin, type 1 - Em
15	76	100.0	370	2 A29664	actin - sea urchin
16	76	100.0	374	1 ATBOB	actin beta - bovin
17	76	100.0	374	1 ATBOG	actin gamma - bovin
18	76	100.0	374	2 JC5818	gamma-actin - huma
19	76	100.0	375	1 ATBOSM	actin, aortic smoo
20	76	100.0	375	1 ATRBB	actin, skeletal mu
21	76	100.0	375	1 ATRTC	actin beta - rat
22	76	100.0	375	1 A48324	actin beta, cytosol
23	76	100.0	375	1 ATAX	actin - Acanthamoeba
24	76	100.0	375	1 ATCHB	actin beta - chick
25	76	100.0	375	1 ATDO	actin - slime mold
26	76	100.0	375	1 ATHUB	actin beta - human
27	76	100.0	375	1 ATHUG	actin gamma 1 - hu
28	76	100.0	375	1 ATMSB	actin beta - mouse
29	76	100.0	375	1 ATMSG	actin gamma - mouse

actin beta, non-mu
actin gamma, cytosol
actin, cytosolic (chicken)
actin 1 - Pneumococcus
hypothetical protein
actin - fission yeast
actin beta-2, cyto
actin beta-1, cyto
actin beta, cytosol
actin beta - goose
actin alpha, cardi
actin - Puccinia graminis
actin - Phaffia rhodolysans
actin - soybean
actin gamma, cytosol
actin - Entamoeba

ALIGNMENTS

RESULT 1

C43616

actin beta, cytosolic - chicken (fragment)

C:Species: Gallus gallus (Chicken)

C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004

C:Accession: C43616

R:Paterson, B.M.; Eldridge, J.D.

Science 224, 1436-1438, 1984

A:Title: alpha-Cardiac actin is the major sarcomeric isoform expressed in embryonic avian muscle

A:Reference number: A43616; MUID:84223949; PMID:6729461

A:Accession: C43616

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-86 <PAT>

A:Cross-references: UNIPROT:Q90736; GB:K02173; NID:g211054; PIDN:AAA98513.1; PID:g211055

C:Superfamily: actin

C:Keywords: cytosol; methylated amino acid

F:73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 76; DB 2; Length 86;

Best Local Similarity 100.0%; Pred. No. 7.1e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLKYP 15

Db 56 DEAQSKRGILTLKYP 70

RESULT 2

A28258

actin 5C - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004

C:Accession: A28258

R:Vigoreaux, J.O.; Tobin, S.L.

Genes Dev. 1, 1161-1171, 1987

A:Title: Stage-specific selection of alternative transcriptional initiation sites from the 5' region of the actin 5C gene

A:Reference number: A28258; MUID:88112795; PMID:3123314

A:Accession: A28258

A:Molecule type: mRNA

A:Residues: 1-137 <VIG>

A:Cross-references: UNIPROT:P10987

A:Note: the authors translated the codon GAG for residue 96 as Gly

C:Genetics:

A:Gene: FlyBase:Act5C

A:Cross-references: FlyBase:FBgn0000042

C:Superfamily: actin

C:Keywords: methylated amino acid

F:74/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 76; DB 2; Length 137;

Best Local Similarity 100.0%; Pred. No. 1.1e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLKYP 15
|||||
Db 57 DEAQSKRGILTLKYP 71

RESULT 3
149465
alpha-cardiac actin - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49465; I49466
R;Garner, I.; Minoy, A.J.; Alonso, S.; Barton, P.J.R.; Buckingham, M.E.
EMBO J. 5, 2559-2567, 1986
A;Title: A 5' duplication of the alpha-cardiac actin gene in BALB/c mice is associated with
A;Reference number: I49465; MUID:87053822; PMID:3023046
A;Accession: I49465
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-158 <RES>
A;Cross-references: UNIPROT:Q61273; GB:M26775; NID:g191646; PIDN:AAA37165.1; PID:g553858
A;Accession: I49466
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 8-158 <RE2>
A;Cross-references: GB:M26776; NID:g191649; PIDN:AAA37166.1; PID:g553859
A;Experimental source: adult cardiac muscle, BALB/c mice
C;Genetics:
A;Introns: 50/3
C;Superfamily: actin
C;Keywords: cardiac muscle; heart

Query Match 100.0%; Score 76; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLKYP 15
|||||
Db 65 DEAQSKRGILTLKYP 79

RESULT 4
S20097
actin 85c - potato (fragment)
C;Species: Solanum tuberosum (potato)
C;Date: 22-Nov-1993 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004
C;Accession: S20097
R;Drouin, G.; Dover, G.A.
J. Mol. Evol. 31, 132-150, 1990
A;Title: Independent gene evolution in the potato actin gene family demonstrated by phylogenetic
A;Reference number: S20092; MUID:91012599; PMID:2120451
A;Accession: S20097
A;Molecule type: DNA
A;Residues: 1-195 <DRO>
A;Cross-references: UNIPROT:P30170; EMBL:X55747; NID:g21541; PIDN:CAA39277.1; PID:g13455
C;Genetics:
A;Introns: 132/1
C;Superfamily: actin
C;Keywords: cytoskeleton; structural protein

Query Match 100.0%; Score 76; DB 2; Length 195;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLKYP 15
|||||
Db 38 DEAQSKRGILTLKYP 52

RESULT 5
A61043
actin CA15 - sea squirt (Styela clava) (fragments)

C;Species: Styela clava
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A61043
R;Beach, R.L.; Jeffery, W.R.
Dev. Genet. 11, 2-14, 1990
A;Title: Temporal and spatial expression of a cytoskeletal actin gene in the ascidian Styela clava
A;Reference number: A61043; MUID:90298580; PMID:2361333
A;Accession: A61043
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-213 <BEA>
A;Cross-references: UNIPROT:Q7M3Y7
C;Comment: This sequence is expressed in cells undergoing rapid cell division.
C;Superfamily: actin
C;Keywords: cytoskeleton; methylated amino acid; mitosis; structural protein
F;73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 76; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLKYP 15
|||||
Db 56 DEAQSKRGILTLKYP 70

RESULT 6
A03000
actin 3 - fruit fly (Drosophila melanogaster) (fragments)
C;Species: Drosophila melanogaster
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C;Accession: A03000
R;Fyrberg, E.A.; Bond, B.J.; Hershey, N.D.; Mixter, K.S.; Davidson, N.
Cell 24, 107-116, 1981
A;Title: The actin genes of Drosophila: protein coding regions are highly conserved but
A;Reference number: A03000; MUID:81210174; PMID:6263481
A;Accession: A03000
A;Molecule type: DNA
A;Residues: 1-308 <FVR>
A;Cross-references: UNIPROT:P02572
A;Note: there are 68 unsequenced residues between positions 160 and 161. Partial sequence
A;Note: the authors translated the codon GTT for residue 263 as Ile
C;Genetics:
A;Gene: FlyBase:Act42A
A;Cross-references: FlyBase:FBgn0000043
A;Map position: 42A
C;Superfamily: actin
C;Keywords: methylated amino acid
F;74/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 76; DB 2; Length 308;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLKYP 15
|||||
Db 57 DEAQSKRGILTLKYP 71

RESULT 7
JC2008
actin homolog protein - red swamp crayfish
C;Species: Procambarus clarkii (red swamp crayfish)
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Jun-2000
C;Accession: JC2008
R;Kang, W.K.; Naye, Y.
Gene 133, 303-304, 1993
A;Title: Sequence of the cDNA encoding an actin homolog in the crayfish Procambarus clarkii
A;Reference number: JC2008; MUID:94040829; PMID:8224920
A;Accession: JC2008
A;Molecule type: mRNA
A;Residues: 1-325 <KAN>
A;Cross-references: GB:D14612; NID:g434784; PIDN:BAA03463.1; PID:g434785

A;Experimental source: muscle
C;Superfamily: actin
C;Keywords: muscle contraction

Query Match 100.0%; Score 76; DB 2; Length 325;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLYP 15
|||||
Db 6 DEAQSKRGILTLYP 20
|||||

RESULT 8

S11452
actin (clone 302) - brine shrimp (fragment)
C;Species: Artemia sp. (brine shrimp)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: S11452

R;Macias, M.T.; Sastre, L.
Nucleic Acids Res. 18, 5219-5225, 1990
A;Title: Molecular cloning and expression of four actin isoforms during Artemia developm
A;Reference number: S11450; MUID:90384823; PMID:2402445
A;Accession: S11452
A;Molecule type: mRNA

A;Residues: 1-327 <MAC>
A;Cross-references: UNIPROT:P18602; EMBL:X52604; NID:G5666; PIDN:CAA36837.1; PID:G829162
C;Superfamily: actin
C;Keywords: methylated amino acid; structural protein
F;25/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 76; DB 2; Length 327;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLYP 15
|||||
Db 8 DEAQSKRGILTLYP 22
|||||

RESULT 9

S05430
actin beta - grass carp
C;Species: Ctenopharyngodon idella (grass carp)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C;Accession: S05430

R;Liu, Z.; Zhu, Z.; Roberg, K.; Faras, A.J.; Guise, K.S.; Kapuscinski, A.R.; Hackett, P.
Nucleic Acids Res. 17, 5850, 1989
A;Title: The beta-actin gene of carp (Ctenopharyngodon idella).
A;Reference number: S05430; MUID:89345185; PMID:2762162

A;Accession: S05430
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-328 <LIU>
A;Cross-references: UNIPROT:P83751; EMBL:M25013
C;Genetics:

A;Introns: 41/3; 121/3; 268/1
C;Superfamily: actin
C;Keywords: cytoskeleton; methylated amino acid
F;73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 76; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLYP 15
|||||
Db 56 DEAQSKRGILTLYP 70
|||||

RESULT 10

B25819
actin, fetal skeletal/adult cardiac muscle - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 09-Jul-2004
C;Accession: B25819
R;Alonso, S.; Minty, A.; Bourlet, Y.; Buckingham, M.

J. Mol. Evol. 23, 11-22, 1986
A;Title: Comparison of three actin-coding sequences in the mouse; evolutionary relations
A;Reference number: A25819; MUID:86200234; PMID:3084797

A;Accession: B25819
A;Molecule type: mRNA
A;Residues: 1-349 <ALO>
A;Cross-references: UNIPROT:Q61275; GB:X03767; GB:J00381; GB:M10652; NID:G49869; PIDN:CF
C;Superfamily: actin
C;Keywords: cardiac muscle; heart; methylated amino acid; muscle; skeletal muscle
F;47/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 76; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLYP 15
|||||
Db 30 DEAQSKRGILTLYP 44
|||||

RESULT 11

S68089
actin 2 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S68089

R;McDowell, J.M.; Huang, S.; McKinney, E.C.; An, Y.Q.; Meagher, R.B.
Genetics 142, 587-602, 1996
A;Title: Structure and evolution of the actin gene family in Arabidopsis thaliana.
A;Reference number: S68089; MUID:96158109; PMID:8852856
A;Accession: S68089

A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-361 <MCD>
A;Cross-references: UNIPROT:Q93ZL9
A;Note: mRNA sequencing was also done
C;Genetics:

A;Gene: ACT2
C;Superfamily: actin
C;Keywords: cytoskeleton; structural protein

Query Match 100.0%; Score 76; DB 2; Length 361;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLYP 15
|||||
Db 53 DEAQSKRGILTLYP 67
|||||

RESULT 12

A26559
actin type 5, cytosolic - chicken
C;Species: Gallus gallus (chicken)

C;Date: 09-Sep-1987 #sequence_revision 09-Sep-1987 #text_change 05-Dec-1997
C;Accession: A26559
R;Bergsma, D.J.; Chang, K.S.; Schwartz, R.J.
Mol. Cell. Biol. 5, 1151-1162, 1985

A;Reference number: A26559; MUID:85213487; PMID:4000121
A;Accession: A26559
A;Molecule type: DNA
A;Residues: 1-362 <BER>

C;Superfamily: actin
C;Keywords: cytosol; methylated amino acid
F;74/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 76; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEAQSKRGILTLYP 15
 |||||
 Db 57 DEAQSKRGILTLYP 71

RESULT 13

S68090
 actin 8 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 05-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C:Accession: S68090
 R:McDowell, J.M.; Huang, S.; McKinney, E.C.; An, Y.Q.; Meagher, R.B.
 Genetics 142, 597-602, 1996
 A:Title: Structure and evolution of the actin gene family in Arabidopsis thaliana.
 A:Reference number: S68089; PMID:96158109; PMID:8852856
 A:Accession: S68090
 A>Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-362 <MCD>
 A:Cross-references: UNIPROT:Q8LB94
 A:Note: mRNA sequencing was also done
 C:Genetics:
 A:Gene: ACT8
 C:Superfamily: actin
 C:Keywords: cytoskeleton; structural protein

Query Match 100.0%; Score 76; DB 2; Length 362;
 Best Local Similarity 100.0%; Pred. No. 3.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEAQSKRGILTLYP 15
 |||||
 Db 54 DEAQSKRGILTLYP 68

RESULT 14

A37431
 actin, type 1 - Emilia huxleyi (fragment)
 C:Species: Emilia huxleyi
 C>Date: 16-Feb-1994 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C:Accession: A37431
 R:Bhattacharya, D.; Stickel, S.K.; Sogin, M.L.
 Mol. Biol. Evol. 10, 689-703, 1993
 A:Title: Isolation and molecular phylogenetic analysis of actin-coding regions from Emilia huxleyi.
 A:Reference number: A37431; PMID:93330051; PMID:7687735
 A:Contents: CCMF379
 A:Accession: A37431
 A>Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-365 <BHA>
 A:Cross-references: UNIPROT:Q41205; GB:S64188; NID:9404406; PIDN:AAB27626.1; PID:G404407
 A:Note: sequence extracted from NCBI backbone (NCBI:135711, NCBI:135712)
 C:Superfamily: actin

Query Match 100.0%; Score 76; DB 2; Length 365;
 Best Local Similarity 100.0%; Pred. No. 3.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEAQSKRGILTLYP 15
 |||||
 Db 46 DEAQSKRGILTLYP 60

RESULT 15

A29664
 actin - sea urchin (Strongylocentrotus purpuratus)
 C:Species: Strongylocentrotus purpuratus (purple urchin)
 C>Date: 15-Dec-1988 #sequence_revision 30-Sep-1991 #text_change 05-Dec-1997
 C:Accession: A29664
 R:Crain Jr.; W.R.; Boshart, M.F.; Cooper, A.D.; Durica, D.S.; Nagy, A.; Steffen, D.
 J. Mol. Evol. 25, 37-45, 1987
 A:Title: The sequence of a sea urchin muscle actin gene suggests a gene conversion with

A:Reference number: A29664; MUID:87311761; PMID:3114500
 A:Accession: A29664
 A:Molecule type: DNA
 A:Residues: 1-370 <CRA>
 A:Cross-references: GB:X05739; GB:X05740; GB:X05741; GB:X05742; GB:X05743
 A:Note: the authors translated the codon CAG for residue 260 as Glu
 C:Superfamily: actin
 C:Keywords: methylated amino acid
 F:73/Modified site: 3'-methylhistidine (His) #status predicted
 Query Match 100.0%; Score 76; DB 2; Length 370;
 Best Local Similarity 100.0%; Pred. No. 3.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DEAQSKRGILTLYP 15
 |||||
 Db 56 DEAQSKRGILTLYP 70
 Search completed: April 8, 2005, 10:53:06
 Job time : 9.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 57.8667 Seconds
(without alignments)
132.739 Million cell updates/sec

Title: US-09-423-351C-9
Perfect score: 76
Sequence: 1 DEAQSKRGILTLYKYP 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	100.0	75	2 Q6KB23	Q6KB23 acipenser s
2	76	100.0	78	2 Q61375	Q61375 schmidtea p
3	76	100.0	78	2 Q61376	Q61376 schmidtea p
4	76	100.0	79	2 Q95L83	Q95L83 oryctolagus
5	76	100.0	80	2 Q9TW4	Q9TW4 bos taurus
6	76	100.0	82	2 Q62788	Q62788 sus scrofa
7	76	100.0	82	2 Q9XSX8	Q9XSX8 bubalus bub
8	76	100.0	86	2 Q90736	Q90736 gallus gall
9	76	100.0	91	2 Q7Z211	Q7Z211 salvelinus
10	76	100.0	94	2 Q8MVN0	Q8MVN0 boltonia vi
11	76	100.0	96	2 Q86CV4	Q86CV4 drosophila
12	76	100.0	96	2 Q86FV7	Q86FV7 drosophila
13	76	100.0	100	2 Q862L0	Q862L0 bos taurus
14	76	100.0	104	2 Q86SB7	Q86SB7 gryllus bim
15	76	100.0	108	2 Q18548	Q18548 lytechinus
16	76	100.0	108	2 Q18550	Q18550 lytechinus
17	76	100.0	117	2 Q8T6P7	Q8T6P7 elysia chlo
18	76	100.0	118	2 Q15593	Q15593 entamoeba h
19	76	100.0	121	2 Q8JG71	Q8JG71 oreochromis
20	76	100.0	121	2 Q8JG71	Q8JG71 oreochromis
21	76	100.0	122	2 Q84IA3	Q84IA3 pseudopleur
22	76	100.0	123	2 Q9SSU4	Q9SSU4 cucumis mel
23	76	100.0	129	2 Q6VBE4	Q6VBE4 locusta mlg
24	76	100.0	130	2 Q93298	Q93298 pseudopleur
25	76	100.0	130	2 Q9DE58	Q9DE58 coryphaenoi
26	76	100.0	139	2 Q3DFK2	Q3DFK2 gillichthys
27	76	100.0	144	2 Q90YX9	Q90YX9 fundulus he
28	76	100.0	147	2 Q7X9B5	Q7X9B5 fragaria an
29	76	100.0	148	2 Q8JIZ5	Q8JIZ5 oncorhynch
30	76	100.0	150	2 Q804Y9	Q804Y9 ictalurus p
31	76	100.0	151	2 Q9AVU2	Q9AVU2 ophioglossu

32	76	100.0	151	2	Q61274	Q61274 mus musculu
33	76	100.0	151	2	Q9PSV5	Q9PSV5 oryzias lat
34	76	100.0	155	2	Q9ZQT0	Q9ZQT0 glycyrrhiza
35	76	100.0	157	2	Q96443	Q96443 glycine max
36	76	100.0	158	2	Q61273	Q61273 mus musculu
37	76	100.0	162	2	Q6UBA0	Q6UBA0 chelonina my
38	76	100.0	164	1	ACT_SPOLI	Q11212 spodoptera
39	76	100.0	164	2	Q6PX70	Q6PX70 capsicum an
40	76	100.0	165	2	Q17477	Q17477 haliothis ru
41	76	100.0	165	2	Q8QFS7	Q8QFS7 scyliorhinu
42	76	100.0	171	2	Q8JHS9	Q8JHS9 chelydra se
43	76	100.0	176	2	Q8PZB5	Q8PZB5 brassica na
44	76	100.0	181	2	Q8JG41	Q8JG41 dicentrarch
45	76	100.0	181	2	Q8AWC8	Q8AWC8 chionodraco

ALIGNMENTS

RESULT 1					
Q6KB23	PRELIMINARY;	PRT;	75 AA.		
AC Q6KB23;					
DT 05-JUL-2004 (Tremblrel. 27, Created)					
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)					
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)					
DE Beta-actin (Fragment).					
OS Acipenser sinensis (Chinese sturgeon).					
OG Chloroplast.					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Actinopterygii; Chondrostei; Acipenseriformes; Acipenseridae;					
OC Acipenser.					
OX NCBI_TaxID=61970;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC TISSUE=Liver;					
RA Zhang Z.;					
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.					
RN [2]					
RP SEQUENCE FROM N.A.					
RC TISSUE=Liver;					
RA Zhaobin Z.;					
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.					
DR EMBL; AJ745100; CAG33738.1; -					
DR GO; GO:0005884; C:actin filament; IEA.					
DR GO; GO:0009507; C:chloroplast; IEA.					
DR GO; GO:0003774; F:motor activity; IEA.					
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.					
DR InterPro; IPR004001; Actin.					
DR PRINTS; PR00190; ACTIN.					
DR PROSITE; PS00406; ACTINS_1; 1.					
KW Chloroplast.					
FT NON TER 1					
FT NON TER 75					
SQ SEQUENCE 75 AA; 8545 MW; 32F1B8CC7C40E388 CRC64;					
Query Match 100.0%; Score 76; DB 2; Length 75;					
Best Local Similarity 100.0%; Pred. No. 2e-06;					
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY 1 DEAQSKRGILTLYKYP 15					
DB 16 DEAQSKRGILTLYKYP 30					
RESULT 2					
Q61375	PRELIMINARY;	PRT;	78 AA.		
ID Q61375					
AC Q61375;					
DT 01-AUG-1998 (Tremblrel. 07, Created)					
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)					
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)					

DE Actin 1 (Fragment).
GN Name=DpAct1.
OS Schmidtea polychroa.
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriate; Tricladida;
OC Paludicola; Dugesidae; Schmidtea.
OX NCBI_TaxID=50054;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=98186847; PubMed=9518500; DOI=10.1093/nar/26.8.2031;
RA Fagotti A., Gabbiani G., Pascolini R., Neuville P.;
RT "Multiple isoform recovery (MIR)-PCR: a simple method for the
RL isolation of related mRNA isoforms.";
RL Nucleic Acids Res. 26:2031-2033(1998).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
CC EMBL; AF027161; AAC38981.1; -.
DR HSSP; P02577; INM1.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0003774; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
DR Structural protein. 78
KW NON TER
FT SEQUENCE 78 AA; 8205 MW; 572BAB2698C24404 CRC64;
SQ

Query Match 100.0%; Score 76; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLYKYP 15
Db 57 DEAQSKRGILTLYKYP 71

RESULT 3
O61376
ID O61376 PRELIMINARY; PRT; 78 AA.
AC O61376;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Actin 2 (Fragment).
GN Name=DpAct2;
OS Schmidtea polychroa.
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriate; Tricladida;
OC Paludicola; Dugesidae; Schmidtea.
OX NCBI_TaxID=50054;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=98186847; PubMed=9518500; DOI=10.1093/nar/26.8.2031;
RA Fagotti A., Gabbiani G., Pascolini R., Neuville P.;
RT "Multiple isoform recovery (MIR)-PCR: a simple method for the
RL isolation of related mRNA isoforms.";
RL Nucleic Acids Res. 26:2031-2033(1998).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
CC EMBL; AF027162; AAC38982.1; -.
DR HSSP; P02577; INM1.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0003774; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.

DR PROSITE; PS00406; ACTINS_1; 1.
KW Structural protein.
FT NON TER 78
SQ SEQUENCE 78 AA; 8265 MW; B9DFF9B28E4ADB0E CRC64;
Query Match 100.0%; Score 76; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLYKYP 15
Db 57 DEAQSKRGILTLYKYP 71

RESULT 4
Q95L83
ID Q95L83 PRELIMINARY; PRT; 79 AA.
AC Q95L83;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta-actin (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=22306422; PubMed=12388084;
RA Wang D.-A., Du H., Jaggar J.H., Brindley D.N., Tigyi G.J.,
RA Watsky M.A.;
RT "Injury-elicited differential transcriptional regulation of
RT phospholipid growth factor receptors in the cornea.";
RL Am. J. Physiol. Cell Physiol. 283:C1646-C1654(2002).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
CC EMBL; AF404278; AAL01885.1; -.
DR HSSP; P02577; INM1.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0003774; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
KW Structural protein.
FT NON TER 79
FT NON TER 79
SQ SEQUENCE 79 AA; 8420 MW; 05056E4E2AC092F8 CRC64;
Query Match 100.0%; Score 76; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLYKYP 15
Db 58 DEAQSKRGILTLYKYP 72

RESULT 5
Q9TW4
ID Q9TW4 PRELIMINARY; PRT; 80 AA.
AC Q9TW4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta actin (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovinae; Bos.
RN [1]_TaxID=9913;
RP SEQUENCE FROM N.A.
RA John S.J., Bilodeau-Goeseels S.; to the EMBL/GenBank/DBJ databases.
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AF191490; AAF05984.1; -.
DR HSSP; P02577; INM1.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
KW Structural protein.
FT NON_TER 1
FT NON_TER 80
SQ SEQUENCE 80 AA; 9133 MW; 47354ABB7010666D CRC64;

Query Match 100.0%; Score 76; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLYKYP 15
Db 22 DEAQSKRGILTLYKYP 36
|||||
RESULT 6
O62788 PRELIMINARY; PRT; 82 AA.
AC O62788;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Beta actin (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99244362; PubMed=10229356;
RA McNeel R.L., Mergmann H.J.;
RT "Distribution and quantification of beta1-, beta2-, and beta3-
RT adrenergic receptor subtype transcripts in porcine tissues."
RL J. Anim. Sci. 77:611-621(1999).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AF054837; AAC08590.1; -.
DR HSSP; P02568; ILCU.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 9410 MW; 8FCC5A5BDAB9F9DC CRC64;

Query Match 100.0%; Score 76; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLYKYP 15
Db 22 DEAQSKRGILTLYKYP 36
|||||
RESULT 6
O62788 PRELIMINARY; PRT; 82 AA.
AC O62788;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Beta actin (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99244362; PubMed=10229356;
RA McNeel R.L., Mergmann H.J.;
RT "Distribution and quantification of beta1-, beta2-, and beta3-
RT adrenergic receptor subtype transcripts in porcine tissues."
RL J. Anim. Sci. 77:611-621(1999).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AF054837; AAC08590.1; -.
DR HSSP; P02568; ILCU.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 9410 MW; 8FCC5A5BDAB9F9DC CRC64;

Query Match 100.0%; Score 76; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLYKYP 15
Db 22 DEAQSKRGILTLYKYP 36
|||||
RESULT 7
Q9XSX8 PRELIMINARY; PRT; 82 AA.
AC Q9XSX8;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Beta actin (Fragment).
OS Bubalus bubalis (Domestic water buffalo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bubalus.
OX NCBI_TaxID=89462;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AF156978; AAD40181.1; -.
DR HSSP; P02577; INM1.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 9417 MW; 9709C6112FAF296C CRC64;

Query Match 100.0%; Score 76; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLYKYP 15
Db 22 DEAQSKRGILTLYKYP 36
|||||
RESULT 8
Q90736 PRELIMINARY; PRT; 86 AA.
AC Q90736;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Beta-actin (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84223949; PubMed=6729461;
RA Paterson B.M., Eldridge J.D.;

RT "alpha-Cardiac actin is the major sarcomeric isoform expressed in
 RL embryonic avian skeletal muscle.";
 CC Science 224:1436-1438(1984).
 CC -!- FUNCTION: Actins are highly conserved proteins that are involved
 CC in various types of cell motility and are ubiquitously expressed
 CC in all eukaryotic cells (By similarity).
 CC -!- SIMILARITY: Belongs to the actin family.
 DR EMBL; K02173; AA98513.1; -.
 DR PIR; C43616; C43616.
 DR HSP; P02577; INM1.
 DR GO; GO:0005884; C:actin filament; IEA.
 DR GO; GO:0003774; F:motor activity; IEA.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
 DR Pfam; PF00022; Actin; 1.
 DR PRINTS; PR00190; ACTIN.
 DR PROSITE; PS00406; ACTINS_1; 1.
 KW Structural protein.
 FT NON TER 86
 SQ SEQUENCE 86 AA; 9351 MW; A55285196A328E6E CRC64;

Query Match 100.0%; Score 76; DB 2; Length 86;
 Best Local Similarity 100.0%; Pred. No. 2.3e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DEAQSKRGILTLYP 15
 |||||
 Db 56 DEAQSKRGILTLYP 70

RESULT 9
 ID Q72Z11 PRELIMINARY; PRT; 91 AA.
 AC Q72Z11;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Beta-actin (Fragment).
 OS Salvelinus alpinus (Arctic char).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 CC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
 OX NCBI_TaxID=8036;
 [1]
 RP SEQUENCE FROM N.A.
 RA McGowan C., Davidson E.A., Davidson W.S.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Actins are highly conserved proteins that are involved
 CC in various types of cell motility and are ubiquitously expressed
 CC in all eukaryotic cells (By similarity).
 CC -!- SIMILARITY: Belongs to the actin family.
 DR EMBL; AY262761; AAP31127.1; -.
 DR HSP; P02577; INM1.
 DR GO; GO:0005884; C:actin filament; IEA.
 DR GO; GO:0003774; F:motor activity; IEA.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
 DR InterPro; IPR004001; Actin.
 DR InterPro; IPR004000; Actin_like.
 DR Pfam; PF00022; Actin; 1.
 DR PRINTS; PR00190; ACTIN.
 DR PROSITE; PS00406; ACTINS_1; 1.
 KW Structural protein.
 FT NON TER 91
 SQ SEQUENCE 91 AA; 10063 MW; 7118DB6663CD895C CRC64;

Query Match 100.0%; Score 76; DB 2; Length 91;
 Best Local Similarity 100.0%; Pred. No. 2.4e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DEAQSKRGILTLYP 15
 |||||
 Db 54 DEAQSKRGILTLYP 69

RESULT 10
 Q8MVNO PRELIMINARY; PRT; 94 AA.
 ID Q8MVNO;
 AC Q8MVNO;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytoskeletal actin 2-like protein (Fragment).
 GN Name=ca2;
 OS Bolitena villosa.
 CC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
 CC Stolidobranchia; Pyuridae; Bolitena.
 OX NCBI_TaxID=63515;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22248966; PubMed=12361966;
 RA Davidson B.J., Swalla B.J.;
 RT "A molecular analysis of ascidian metamorphosis reveals activation of
 RT an innate immune response";
 RL Development 129:4739-4751(2002).
 CC -!- FUNCTION: Actins are highly conserved proteins that are involved
 CC in various types of cell motility and are ubiquitously expressed
 CC in all eukaryotic cells (By similarity).
 CC -!- SIMILARITY: Belongs to the actin family.
 DR EMBL; AF483031; AAM76111.1; -.
 DR HSP; P02577; INM1.
 DR GO; GO:0005884; C:actin filament; IEA.
 DR GO; GO:0003774; F:motor activity; IEA.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
 DR InterPro; IPR004001; Actin.
 DR InterPro; IPR004000; Actin_like.
 DR Pfam; PF00022; Actin; 1.
 DR PRINTS; PR00190; ACTIN.
 DR PROSITE; PS00406; ACTINS_1; 1.
 KW Structural protein.
 FT NON TER 94
 SQ SEQUENCE 94 AA; 10576 MW; 6CEAB58DA12372A4 CRC64;

Query Match 100.0%; Score 76; DB 2; Length 94;
 Best Local Similarity 100.0%; Pred. No. 2.5e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLYP 15
 |||||
 Db 41 DEAQSKRGILTLYP 55

RESULT 11
 Q86CV4 PRELIMINARY; PRT; 96 AA.
 ID Q86CV4;
 AC Q86CV4;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Actin E2 (Fragment).
 GN Name=ActE2;
 OS Drosophila novamexicana.
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=47314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=15010-1031.0;
 RX MEDLINE=22480340; PubMed=12574518; DOI=10.1073/pnas.0336368100;
 RA Wittkopp P.J., Williams B.L., Selegue J.E., Carroll S.B.;
 RT "Drosophila pigmentation evolution: divergent genotypes underlying
 RT convergent phenotypes";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1808-1813(2003).
 CC -!- FUNCTION: Actins are highly conserved proteins that are involved
 CC in various types of cell motility and are ubiquitously expressed
 CC in all eukaryotic cells (By similarity).

-!- SIMILARITY: Belongs to the actin family.

CC EMBL; AY165541; AAC21565.1; -;
 DR HSSP; P02568; ILCU.
 DR FlyBase; FBgn0066214; Dnov\ActE2.
 DR GO; GO:0005884; C:actin filament; IEA.
 DR GO; GO:0003774; F:motor activity; IEA.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
 DR InterPro; IPR004001; Actin.
 DR InterPro; IPR004001; Actin_like.
 DR Pfam; PF00022; Actin; 1.
 DR PRINTS; PR00190; ACTIN.
 DR PROSITE; PS00406; ACTINS_1; 1.
 KW Structural protein.
 FT NON_TER 96
 SQ SEQUENCE 96 AA; 10610 MW; 1454B7D9DD3F3564 CRC64;

Query Match 100.0%; Score 76; DB 2; Length 96;
 Best Local Similarity 100.0%; Pred. No. 2.5e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLYP 15

Db 57 DEAQSKRGILTLYP 71

RESULT 12

Q86FV7 PRELIMINARY; PRT; 96 AA.

ID Q86FV7
 AC Q86FV7
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Actin E2 (Fragment).
 GN Name=ActE2;
 OS Drosophila americana (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=40366;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=15010-0951.0;
 RX MEDLINE=22480340; PubMed=12574518; DOI=10.1073/pnas.0336368100;
 RA Wittkopp P.J., Williams B.L., Selegue J.E., Carroll S.B.;
 RT "Drosophila pigmentation evolution: divergent genotypes underlying
 convergent phenotypes".
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1808-1813(2003).
 CC -!- FUNCTION: Actins are highly conserved proteins that are involved
 in various types of cell motility and are ubiquitously expressed
 in all eukaryotic cells (By similarity).
 CC -!- SIMILARITY: Belongs to the actin family.

CC EMBL; AY165516; AAP12711.1; -;
 DR HSSP; P02568; ILCU.
 DR FlyBase; FBgn0066281; Dame\ActE2.
 DR GO; GO:0005884; C:actin filament; IEA.
 DR GO; GO:0003774; F:motor activity; IEA.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
 DR InterPro; IPR004001; Actin.
 DR InterPro; IPR004000; Actin_like.
 DR Pfam; PF00022; Actin; 1.
 DR PRINTS; PR00190; ACTIN.
 DR PROSITE; PS00406; ACTINS_1; 1.
 KW Structural protein.
 FT NON_TER 96
 SQ SEQUENCE 96 AA; 10610 MW; 1454B7D9DD3F3564 CRC64;

Query Match 100.0%; Score 76; DB 2; Length 96;
 Best Local Similarity 100.0%; Pred. No. 2.5e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLYP 15

Db 57 DEAQSKRGILTLYP 71

RESULT 13

Q862L0 PRELIMINARY; PRT; 100 AA.

ID Q862L0
 AC Q862L0
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Similar to b-actin (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22544902; PubMed=12658628; DOI=10.1002/mrd.10292;
 RA Ishiwata H., Katsuma S., Kizaki K., Patel O.V., Nakano H.,
 RA Takahashi T., Inai K., Hirasawa A., Shiojima S., Ikawa H., Suzuki Y.,
 RA Tsujimoto G., Izaike Y., Todoroki J., Hashizume K.;
 RT "Characterization of gene expression profiles in early bovine
 pregnancy using a custom cDNA microarray.";
 RL Mol. Reprod. Dev. 65:9-18(2003).
 CC -!- FUNCTION: Actins are highly conserved proteins that are involved
 in various types of cell motility and are ubiquitously expressed
 in all eukaryotic cells (By similarity).
 CC -!- SIMILARITY: Belongs to the actin family.

CC EMBL; AB098974; BAC56464.1; -;
 DR HSSP; P02568; IP8Z.
 DR GO; GO:0005884; C:actin filament; IEA.
 DR GO; GO:0003774; F:motor activity; IEA.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
 DR InterPro; IPR004001; Actin.
 DR InterPro; IPR004000; Actin_like.
 DR Pfam; PF00022; Actin; 1.
 DR PRINTS; PR00190; ACTIN.
 DR PROSITE; PS00406; ACTINS_1; 1.
 DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
 KW Structural protein.
 FT NON_TER 1
 FT NON_TER 100
 SQ SEQUENCE 100 AA; 11601 MW; 0E1467471D0019D CRC64;

Query Match 100.0%; Score 76; DB 2; Length 100;
 Best Local Similarity 100.0%; Pred. No. 2.6e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLYP 15

Db 19 DEAQSKRGILTLYP 33

RESULT 14

Q86SB7 PRELIMINARY; PRT; 104 AA.

ID Q86SB7
 AC Q86SB7
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Actin (Fragment).
 GN Name=ACT;
 OS Gryllus bimaculatus (Two-spotted cricket).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
 OC Gryllus.
 OX NCBI_TaxID=6999;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX Zhang H., Shimmyo Y., Hirose A., Mito T., Inoue Y., Ohuchi H.,
 RA Loukeris T.G., Noji S.;
 RT "Extrachromosomal transposition of the transposable element Minos
 occurs in embryos of the cricket Gryllus bimaculatus.";

RL Dev. Growth Differ. 0:0-0(2002).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AB087882; BAC55093.1; -.
DR HSSP; P02577; 1NM1.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
KW Structural protein.
FT NON_TER 104
SQ SEQUENCE 104 AA; 11511 MW; 332777A2B08669B0 CRC64;

Query Match 100.0%; Score 76; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.7e-06; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEAQSKRGILTLYP 15
DB 57 DEAQSKRGILTLYP 71
|||||

RESULT 15
O18548
ID O18548 PRELIMINARY; PRT; 108 AA.
AC O18548;
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Cytoplasmic actin Lvc4 (Fragment).
GN Name=Lvc4;
OS Lytechinus variegatus (Sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Temnopleuroidea; Toxopneustidae;
OC Lytechinus.
OX NCBI_TaxID=7654;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97333945; PubMed=9190067;
RX Kieseinger J.C., Hahn J.H., Raff R.A.;
RT "Rapid evolution in a conserved gene family. Evolution of the actin
RT gene family in the sea urchin genus Helicodaris and related genera."
RL Mol. Biol. Evol. 14:654-665(1997).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; U82542; AAB66299.1; -.
DR HSSP; P10983; 1D4X.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON_TER 1
SQ SEQUENCE 108 AA; 12094 MW; F670CB8A6CBD3AEA CRC64;

Query Match 100.0%; Score 76; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.8e-06; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEAQSKRGILTLYP 15
DB 43 DEAQSKRGILTLYP 57
|||||
Search completed: April 8, 2005, 12:03:12
Job time : 58.8667 secs

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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 62.4 seconds
(without alignments)
92.971 Million cell updates/sec

Title: US-09-423-351C-10

Perfect score: 71

Sequence: 1 IQAVLSLYASGRITG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71	100.0	15	2 AAW92536	Beta-acti
2	71	100.0	97	4 AAM13687	Peptide #
3	71	100.0	97	4 ABB32618	Peptide #
4	71	100.0	97	4 AAM26087	Peptide #
5	71	100.0	97	4 ABB27467	Human pep
6	71	100.0	97	4 ABB18116	Protein #
7	71	100.0	97	4 AAM65825	Human bon
8	71	100.0	97	4 AAM53448	Human bra
9	71	100.0	97	4 ABB47471	Human liv
10	71	100.0	97	4 AAM01437	Peptide #
11	71	100.0	97	5 ABB35459	Human pep
12	71	100.0	137	4 AAU33076	Novel hum
13	71	100.0	150	4 ABB15101	Novel hum
14	71	100.0	157	4 ABB66853	Drosophil
15	71	100.0	166	4 ABB26869	Novel hum
16	71	100.0	168	5 ABB42912	Human ova
17	71	100.0	183	5 ABB42300	Human ova
18	71	100.0	185	6 ABB70840	Human ova
19	71	100.0	196	6 ABB70816	Human adi
20	71	100.0	204	5 ABB43016	Human ova
21	71	100.0	211	7 ABB73899	DNA clone
22	71	100.0	239	7 ABB31206	Human dia
23	71	100.0	257	3 AAG37992	Arabidops
24	71	100.0	257	3 AAG20916	Arabidops
25	71	100.0	274	6 ABB70549	Human adi

26	71	100.0	276	3 AAG50947	Arabidops
27	71	100.0	277	3 AAG05115	Arabidops
28	71	100.0	294	3 AAG20915	Arabidops
29	71	100.0	294	3 AAG37991	Arabidops
30	71	100.0	294	7 ADL63068	Human apo
31	71	100.0	295	3 AAG20914	Arabidops
32	71	100.0	295	3 AAG37990	Arabidops
33	71	100.0	304	3 AAG50946	Arabidops
34	71	100.0	305	3 AAG05114	Arabidops
35	71	100.0	308	3 AAG37210	Arabidops
36	71	100.0	311	3 AAG37209	Arabidops
37	71	100.0	321	3 AAG50945	Arabidops
38	71	100.0	322	3 AAG05113	Arabidops
39	71	100.0	332	3 AAG06448	Arabidops
40	71	100.0	332	3 AAG50873	Arabidops
41	71	100.0	332	3 AAG07390	Arabidops
42	71	100.0	332	3 AAG41511	Arabidops
43	71	100.0	332	3 AAG37989	Arabidops
44	71	100.0	332	3 AAG37317	Arabidops
45	71	100.0	332	3 AAG44697	Zea mays

ALIGNMENTS

RESULT 1
AAW92536
ID AAW92536 standard; peptide; 15 AA.
XX AC AAW92536;
XX 26-APR-1999 (first entry)
DT Beta-actin reference peptide substrate #10.
DE Peptide substrate; CCT; eukaryotic type II chaperonin complex; cyclin;
KW binding agent; substrate-binding site; SBS; substrate folding; actin;
KW tubulin; treatment; cancer; anticancer drug; viral infection; screening;
KW reduced toxicity.
XX Synthetic.
XX WO9853322-A1.
XX 26-NOV-1998.
PD 22-MAY-1998; 98WO-GB001485.
PF 23-MAY-1997; 97GB-00010762.
XX (CANC-) INST CANCER RES ROYAL CANCER HOSPITAL.
XX Willison K, Hynes G, Liou AK;
WPI; 1999-070162/06.
PT Identifying specific binding agents for substrate binding site in CCT
PT chaperonin complex - also new peptide binding agents and their mimetics,
and peptides containing a specific CCT binding site, used for treating
cancer.
PS Disclosure; Fig 10; 97pp; English.
CC This invention describes a method which uses the CCT (eukaryotic type II
chaperonin) complex or part of it, for identifying a binding agent that
can occupy a substrate-binding site (SBS) on the CCT complex. By binding
to the CCT complex, the binding agents block an SBS so that biological
activity of the CCT complex is affected, particularly its ability to fold
substrates such as actin, tubulin and cyclin. The binding agents are
useful for treatment of cancer, particularly when used in combination
with an anticancer drug, or viral infections. Nucleic acid fragments are
used to screen for agents, e.g. binding agents that modulate interaction
between the CCT complex and a protein that is to be folded. The binding

CC agents may target cells that are actively synthesizing tubulin etc.
 CC (unlike known microtubule-stabilising agents that affect all cells), so
 CC should have reduced toxicity for normal cells. AAM92527-W92541 are
 CC peptide substrates used in the method of the invention
 XX
 XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 71; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 8.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 IQAVLSLYASGRRTTG 15
 |||||
 Db 1 IQAVLSLYASGRRTTG 15
 |||||

RESULT 2
 AAM13687
 ID AAM13687 standard; protein; 97 AA.
 XX
 AC AAM13687;
 XX
 XX

DT 12-OCT-2001 (first entry)
 XX Peptide #121 encoded by probe for measuring cervical gene expression.
 DE Probe; human; microarray; gene expression; cervical epithelial cell;
 KW cervical cancer.
 XX Homo sapiens.
 OS
 XX WO200157278-A2.
 PN
 XX 09-AUG-2001.
 XX
 XX

PI 30-JAN-2001; 2001WO-US000670.
 XX
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488901/53.
 DR
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human cervical epithelial cells.
 XX
 PS Claim 27; SEQ ID NO 18513; 487pp; English.

CC The present invention relates to human single exon nucleic acid probes
 CC (SENPs: see AAI10068-AAI28459). The present sequence is a peptide encoded
 CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
 CC can be used to produce a single exon microarray, which can be used for
 CC measuring human gene expression in a sample derived from human cervical
 CC epithelial cells. By measuring gene expression, the probes are therefore
 CC useful in grading and/or staging of diseases of the cervix, notably
 CC cervical cancer. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX SQ Sequence 97 AA;

Query Match 100.0%; Score 71; DB 4; Length 97;
 Best Local Similarity 100.0%; Pred. No. 7.6e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 IQAVLSLYASGRRTTG 15
 |||||
 Db 15 IQAVLSLYASGRRTTG 29
 |||||

RESULT 3
 ABB32618
 ID ABB32618 standard; peptide; 97 AA.
 XX
 AC ABB32618;
 XX
 XX 04-FEB-2002 (first entry)
 XX

DE Peptide #124 encoded by human foetal liver single exon probe.
 XX Human; foetal liver; gene expression; single exon nucleic acid probe.
 XX Homo sapiens.
 OS
 XX WO200157277-A2.
 PN
 XX 09-AUG-2001.
 XX
 XX 30-JAN-2001; 2001WO-US000669.
 XX

PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-483447/52.
 DR
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human foetal liver.
 XX
 PS Claim 27; SEQ ID NO 25253; 639pp + Sequence Listing; English.

CC The invention relates to a single exon nucleic acid probe for measuring
 CC human gene expression in a sample derived from human foetal liver. The
 CC single exon nucleic acid probes may be used for predicting, measuring and
 CC displaying gene expression in samples derived from human foetal liver. The
 CC present sequence is a peptide encoded by a single exon nucleic acid probe
 CC of the invention. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX SQ Sequence 97 AA;

Query Match 100.0%; Score 71; DB 4; Length 97;
 Best Local Similarity 100.0%; Pred. No. 7.6e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 IQAVLSLYASGRRTTG 15
 |||||
 Db 15 IQAVLSLYASGRRTTG 29
 |||||

RESULT 4
 AAM26087
 ID AAM26087 standard; protein; 97 AA.
 XX
 AC AAM26087;
 XX

DT 17-OCT-2001 (first entry)
 XX Peptide #124 encoded by probe for measuring placental gene expression.
 XX

XX Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.
XX Homo sapiens.

OS WO200157272-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000663.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human placenta.

XX Claim 27; SEQ ID NO 26356; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENP;

XX see AA131315-AA157546). The present sequence is a peptide encoded by one

XX such probe. The probes are useful for producing a microarray for

XX predicting, measuring and displaying gene expression in samples derived

XX from human placenta. The probes are useful for antenatal diagnosis of

XX human genetic disorders

XX Sequence 97 AA;

Query Match 100.0%; Score 71; DB 4; Length 97;

Best Local Similarity 100.0%; Pred. No. 7.6e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IQAVLSLYASGRRTG 15

Db 15 IQAVLSLYASGRRTG 29

RESULT 5

ABB27467

ID ABB27467 standard; peptide; 97 AA.

XX ABB27467;

XX 01-FEB-2002 (first entry)

XX Human peptide #118 encoded by breast cell single exon nucleic acid probe.

XX Human; microarray; single exon probe; gene expression; breast; disease;

XX cancer.

XX Homo sapiens.

XX WO200157271-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000662.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-496933/54.

XX New spatially-addressable set of single exon nucleic acid probes, useful

XX for measuring gene expression in sample derived from human breast,

XX comprises number of single exon nucleic acid probes.

XX Claim 27; SEQ ID NO 10435; 327pp + Sequence Listing; English.

XX The invention relates to a spatially-addressable set of single exon

XX nucleic acid probes for measuring gene expression in a sample derived

XX from human breast and BT 474 cells. The method involves contacting the

XX probes with a collection of detectably labelled nucleic acids derived

XX from mRNA of human breast, and then measuring the label bound to each

XX probe of the microarray. The probes are useful for verifying the

XX expression of regions of genomic DNA predicted to encode proteins. They

XX are useful for gene discovery, and for determining predisposition and/or

XX assessing breast disease. Gene expression analysis is useful for

XX this invention presents a far greater diversity of probes for measuring

XX gene expression, with far less bias than expressed sequence tag

XX microarrays. The method is suitable for rapid production of functional

XX information from genomic sequence. The present sequence is a peptide

XX encoded by a single exon nucleic acid probe of the invention. Note: The

XX sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from WIPO

XX at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 97 AA;

Query Match 100.0%; Score 71; DB 4; Length 97;

Best Local Similarity 100.0%; Pred. No. 7.6e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IQAVLSLYASGRRTG 15

Db 15 IQAVLSLYASGRRTG 29

RESULT 6

ABB18116

ID ABB18116 standard; protein; 97 AA.

XX ABB18116;

XX 23-JAN-2002 (first entry)

XX Protein #115 encoded by probe for measuring heart cell gene expression.

XX Human; gene expression; heart; microarray; vascular system;

XX cardiovascular disease; hypertension; cardiac arrhythmia;

XX congenital heart disease.

XX Homo sapiens.

XX WO200157274-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000666.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488899/53.
 XX Single exon nucleic acid probes for analyzing gene expression in human
 PT hearts.
 XX
 XX Claim 15; SEQ ID NO 19886; 530pp; English.
 XX
 XX The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart (see
 CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
 CC probe. The probes may be used for predicting, measuring and displaying
 CC gene expression in samples derived from the human heart via microarrays.
 CC By measuring gene expression, the probes are useful for predicting,
 CC diagnosing, grading, staging, monitoring and prognosing diseases of the
 CC human heart and vascular system e.g. cardiovascular disease,
 CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 97 AA;
 SQ
 Query Match 100.0%; Score 71; DB 4; Length 97;
 Best Local Similarity 100.0%; Pred. NO. 7.6e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IQAVLSLYASGRITG 15
 DB 15 IQAVLSLYASGRITG 29
 RESULT 7
 AAM65825
 ID AAM65825 standard; protein; 97 AA.
 XX
 XX AAM65825;
 AC
 XX
 XX 06-NOV-2001 (first entry)
 DT
 XX
 XX Human bone marrow expressed probe encoded protein SEQ ID NO: 26131.
 DE
 XX Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukaemia; lymphoma; myeloma.
 KW
 XX Homo sapiens.
 OS
 XX WO200157276-A2.
 PN
 XX 09-AUG-2001.
 PD
 XX
 XX 30-JAN-2001; 2001WO-US000668.
 PF
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI
 XX WPI; 2001-488900/53.
 XX

XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human bone marrow.
 PR
 XX Example 4; SEQ ID NO 26131; 658pp + Sequence Listing; English.
 PS
 XX The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a
 CC protein encoded by one of the probes of the invention
 XX
 XX Sequence 97 AA;
 SQ
 Query Match 100.0%; Score 71; DB 4; Length 97;
 Best Local Similarity 100.0%; Pred. NO. 7.6e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IQAVLSLYASGRITG 15
 DB 15 IQAVLSLYASGRITG 29
 RESULT 8
 AAM53448
 ID AAM53448 standard; protein; 97 AA.
 XX
 XX AAM53448;
 AC
 XX
 XX 05-NOV-2001 (first entry)
 DT
 XX
 XX Human brain expressed single exon probe encoded protein SEQ ID NO: 25553.
 DE
 XX Human; brain expressed exon; gene expression analysis; probe; microarray;
 KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
 KW
 XX Homo sapiens.
 OS
 XX WO200157275-A2.
 PN
 XX 09-AUG-2001.
 PD
 XX
 XX 30-JAN-2001; 2001WO-US000667.
 PF
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI
 XX WPI; 2001-483446/52.
 XX
 XX Single exon nucleic acid probes for analyzing gene expression in human
 PT brains.
 XX
 XX Example 4; SEQ ID NO 25553; 650pp + Sequence Listing; English.
 PS
 XX The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancers. The present sequence is a protein encoded by one of
 CC the probes of the invention
 XX
 XX Sequence 97 AA;
 SQ

Query Match 100.0%; Score 71; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 7.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRRTTG 15
DB 15 IQAVLSLYASGRRTTG 29
|||||

RESULT 9
ABG47471
ID ABG47471 standard; peptide; 97 AA.

XX AC ABG47471;
DT 25-FEB-2003 (first entry)
XX DE Human liver peptide, SEQ ID No 26119.
XX KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
XX KW hypercholesterolaemia; coronary heart disease.
XX OS Homo sapiens.

XX WO200157273-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000664.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488898/53.

XX DR Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human adult liver.
XX PS Claim 27; SEQ ID NO 26119; 658pp; English.
XX CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
XX CC measuring human gene expression in a sample derived from human adult
XX CC liver, comprising one of 13109 defined nucleotide sequences given in the
XX CC specification (or complements/ fragments). The probe hybridises at high
XX CC stringency to a nucleic acid molecule expressed in the human adult liver.
XX CC (I) may be used for predicting, measuring and displaying gene expression
XX CC in samples derived from human adult liver. The genes identified may be
XX CC involved in genetic liver diseases such as cirrhosis,
XX CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
XX CC associated with coronary heart disease. ABG47348-ABG5930 represent human
XX CC liver single exon encoded peptides of the invention. Note: The sequence
XX CC information for this patent does not appear in the printed specification
XX CC but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 97 AA;

Query Match 100.0%; Score 71; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 7.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRRTTG 15
DB 15 IQAVLSLYASGRRTTG 29
|||||

RESULT 11
ABG35459
ID ABG35459 standard; peptide; 97 AA.

XX AC ABG35459;
XX AC ABG35459;

DB 15 IQAVLSLYASGRRTTG 29
RESULT 10
AAW01437
ID AAW01437 standard; protein; 97 AA.
XX AC AAW01437;
XX DT 09-OCT-2001 (first entry)

XX DE Peptide #119 encoded by probe for measuring human breast gene expression.
XX KW Probe; human; breast disease; breast cancer; development disorder;
XX KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX OS Homo sapiens.

XX WO200157270-A2.

XX PD 09-AUG-2001.

XX PF 29-JAN-2001; 2001WO-US000661.

XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-476286/51.

XX DR Novel single exon nucleic acid probe used to measuring gene expression in
XX PT a human breast.
XX PS Claim 27; SEQ ID NO 10177; 322pp; English.
XX CC The present invention relates to novel single exon nucleic acid probes
XX CC (see AAI00010-AAI10067). The present sequence is a peptide encoded by one
XX CC such probe. The probes are useful for measuring human gene expression in
XX CC a human breast sample, where the probe hybridises at high stringency to a
XX CC nucleic acid expressed in the human breast. The probes are useful for
XX CC predicting, diagnosing, grading, staging, monitoring and prognosing
XX CC diseases of the human breast, particularly those diseases with polygenic
XX CC aetiology. The diseases include: breast cancer, disorders of polycystic
XX CC inflammatory diseases of the breast, fibrocystic changes, proliferative
XX CC breast disease and non-carcinoma tumours. Note: The sequence data for
XX CC this patent did not form part of the printed specification, but was
XX CC obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 97 AA;

Query Match 100.0%; Score 71; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 7.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRRTTG 15
DB 15 IQAVLSLYASGRRTTG 29
|||||

RESULT 11
ABG35459
ID ABG35459 standard; peptide; 97 AA.

XX AC ABG35459;
XX AC ABG35459;

CC histiocytosis, lymphangioliomyomatosis, pulmonary alveolar proteinosis,
CC Karsenger syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC present sequence is a peptide/protein encoded by a single exon probe of
CC the invention. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 97 AA;

Query Match 100.0%; Score 71; DB 5; Length 97;
Best Local Similarity 100.0%; Pred. No. 7.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRRTG 15
||| ||||| ||||| |||||
DB 15 IQAVLSLYASGRRTG 29

RESULT 12
AAU33076
ID AAU33076 standard; protein; 137 AA.
XX
XX AAU33076;
XX AC
XX AC
XX DT
XX DT
XX DT
DE Novel human secreted protein #3567.
XX
XX Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
XX Homo sapiens.
OS
XX
XX WO200179449-A2.
PN
XX
XX 25-OCT-2001.
XX
XX 16-APR-2001; 2001WO-US008656.
XX
XX 18-APR-2000; 2000US-00552929.
PR
PR 26-JAN-2001; 2001US-00770160.
XX
XX (HYSE-) HYSEQ INC.
XX
XX
XX Tang YT, Liu C, Drmanac RT;
PI
XX
XX WPI; 2001-611725/70.
DR
XX
XX Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy.
PT
XX
XX
XX Claim 20; Page 704-705; 765pp; English.
PS
XX
XX The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising the
CC nucleic acids encoding the polypeptides and cells genetically engineered
CC to express them are also useful for producing the proteins. The proteins
CC are useful in genetic vaccination, testing and therapy, and can be used
CC as nutritional supplements. They may be used to increase stem cell
CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
CC and/or nerve tissue growth or regeneration; immune suppression and/or
CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
CC AAU29510-AAU33304 represent the amino acid sequences of novel human
CC secreted proteins of the invention
XX
XX

Sequence 150 AA;

```

XX 18-FEB-2002 (first entry)
XX
XX
XX
XX Novel human diagnostic protein #26860.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX PD 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
XX
XX 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI: 2001-639362/73.
XX
XX N-PSDB; AAS91056.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX
XX Claim 20; SEQ ID NO 57228; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activity. The
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
XX amino acid sequences of the invention. Note: The sequence data for this
XX patent did not appear in the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 166 AA;
XX
XX Query Match 100.0%; Score 71; DB 4; Length 166;
XX Best Local Similarity 100.0%; Pred. NO. 0.00015;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 IQAVLSLYASGRTTG 15
XX
XX DB 147 IQAVLSLYASGRTTG 161
XX
XX Search completed: April 8, 2005, 10:50:48
XX Job time : 62.4 secs

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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:57 ; Search time 17.5333 Seconds
(without alignments)
63.863 Million cell updates/sec

Title: US-09-423-351C-10

Perfect score: 71

Sequence: 1 IQAVLSLYASGRRTTG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/1aa/5A COMB.pdp.*
- 2: /cgn2_6/ptodata/1/1aa/5B COMB.pdp.*
- 3: /cgn2_6/ptodata/1/1aa/6A COMB.pdp.*
- 4: /cgn2_6/ptodata/1/1aa/6B COMB.pdp.*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS COMB.pdp.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	100.0	336	4	US-09-248-796A-14108
2	71	100.0	371	1	US-08-261-206A-77
3	71	100.0	374	3	US-08-609-236-6
4	71	100.0	375	2	US-08-494-151-14
5	71	100.0	375	3	US-09-106-217-16
6	71	100.0	375	3	US-09-171-337A-7
7	71	100.0	375	3	US-09-171-337A-8
8	71	100.0	375	4	US-09-631-022-7
9	71	100.0	375	4	US-09-631-022-8
10	71	100.0	375	4	US-09-976-594-731
11	71	100.0	376	1	US-08-588-113-2
12	71	100.0	376	4	US-09-949-016-6100
13	71	100.0	377	3	US-09-106-217-2
14	71	100.0	377	4	US-09-919-172-33
15	71	100.0	377	4	US-09-917-254-53
16	71	100.0	386	4	US-09-949-016-7721
17	71	100.0	399	4	US-09-949-016-9424
18	71	100.0	402	4	US-09-949-016-10757
19	71	100.0	404	4	US-09-949-016-11313
20	68	95.8	377	4	US-09-248-796A-14109
21	65	91.5	146	3	US-09-306-446C-5
22	65	91.5	362	4	US-09-949-016-7725
23	65	91.5	374	3	US-09-306-446C-2
24	65	91.5	376	4	US-09-538-092-1109
25	65	91.5	376	4	US-09-538-092-1110
26	65	91.5	376	4	US-09-949-016-6656
27	65	91.5	376	4	US-09-949-016-8452

28	62	87.3	384	4	US-09-538-092-395	Sequence 395, Appl
29	51	71.8	394	4	US-09-949-016-6655	Sequence 6655, Ap
30	51	71.8	406	4	US-09-949-016-7396	Sequence 7396, Ap
31	44	62.0	3816	3	US-09-428-517-3	Sequence 3, Appli
32	44	62.0	4150	3	US-09-428-517-2	Sequence 2, Appli
33	39	54.9	888	4	US-09-697-022-4	Sequence 4, Appli
34	39	54.9	888	4	US-09-697-022-5	Sequence 5, Appli
35	39	54.9	6396	4	US-09-410-551B-72	Sequence 72, Appl
36	39	54.9	6396	4	US-09-940-316B-72	Sequence 72, Appl
37	38	53.5	138	4	US-09-107-532A-6906	Sequence 6906, Ap
38	38	53.5	389	4	US-09-270-767-39072	Sequence 39072, A
39	38	53.5	389	4	US-09-270-767-54289	Sequence 54289, A
40	38	53.5	953	3	US-09-245-281-43	Sequence 43, Appl
41	38	53.5	953	4	US-09-207-359B-43	Sequence 43, Appl
42	38	53.5	953	4	US-09-340-620A-43	Sequence 43, Appl
43	38	53.5	953	4	US-09-865-364-43	Sequence 43, Appl
44	38	53.5	966	4	US-09-207-339B-47	Sequence 47, Appl
45	38	53.5	966	4	US-09-865-364-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1

US-09-248-796A-14108
; Sequence 14108, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 14108
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-14108

Query Match 100.0%; Score 71; DB 4; Length 336;
Best Local Similarity 100.0%; Pred. No. 7.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 IQAVLSLYASGRRTTG 15

Db 69 IQAVLSLYASGRRTTG 83

RESULT 2

US-08-261-206A-77
; Sequence 77, Application US/08261206A
; Patent No. 5574007
; GENERAL INFORMATION:
; APPLICANT: Zushi, Mitichitaka
; APPLICANT: Gomi, Komakazu
; APPLICANT: Yamamoto, Shuji
; APPLICANT: Suzuki, Koji
; APPLICANT: Matsuda, Akio
; TITLE OF INVENTION: A Polypeptide Capable of Interacting
; TITLE OF INVENTION: with Thrombin
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 301 N. Washington St.
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA

ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/261,206A
FILING DATE: 03-AUG-1991
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 07/740,492
FILING DATE: 03-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30330
REFERENCE/DOCKET NUMBER: 216-275P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
TYPE: amino acid
MOLECULE TYPE: linear
US-08-261-206A-77

Query Match 100.0%; Score 71; DB 1; Length 371;
Best Local Similarity 100.0%; Pred. No. 8.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IQAVLSLYASGRRTG 15
Db 134 IQAVLSLYASGRRTG 148

RESULT 3
US-08-609-236-6
Sequence 6, Application US/08609236
Patent No. 6087398
GENERAL INFORMATION:
APPLICANT: Steven R. Goodman
TITLE OF INVENTION: No. 6087398el Sickie Cell Anemia Treatment
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: McGregor & Adler, LLP
STREET: 8011 Candle Lane
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,236
FILING DATE: March 1, 1996
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: 60/002,288
FILING DATE: August 14, 1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5807
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
TELEFAX: 713-777-6908

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 374
TYPE: Amino acid
STRANDEDNESS:
TOPOLOGY: Linear
MOLECULE TYPE: Protein
DESCRIPTION: Protein
HYPOTHETICAL: No
ANTI-SENSE: No
FRAGMENT TYPE:
ORIGINAL SOURCE:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
US-08-609-236-6

Query Match 100.0%; Score 71; DB 3; Length 374;
Best Local Similarity 100.0%; Pred. No. 8.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IQAVLSLYASGRRTG 15
Db 135 IQAVLSLYASGRRTG 149

RESULT 4
US-08-494-151-14
Sequence 14, Application US/08494151
Patent No. 5840528
GENERAL INFORMATION:
APPLICANT: Van Ooyen, Albert Johannes Joseph
TITLE OF INVENTION: Transformation of Phaffia rhodozyma
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,151
FILING DATE: 23-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20039.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-494-151-14

Query Match 100.0%; Score 71; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 8.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IQAVLSLYASGRRTG 15

Db 136 IQAVLSLYASGRRTG 150
|||||

RESULT 5

US-09-106-217-16
; Sequence 16, Application US/09106217
; Patent No. 6063576

GENERAL INFORMATION:

APPLICANT: Keating, Mark T.

APPLICANT: Olson, Timothy M.

TITLE OF INVENTION: Actin Mutations in Dilated

TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.

STREET: 555 Thirteenth Street, N.W., Suite 701 East

CITY: Washington

STATE: DC

COUNTRY: U.S.A.

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/106,217

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Saxe, Stephen A.

REGISTRATION NUMBER: 38,609

REFERENCE/DOCKET NUMBER: 2323-125

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-783-6040

TELEFAX: 202-783-6031

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 375 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-106-217-16

Query Match 100.0%; Score 71; DB 3; Length 375;

Best Local Similarity 100.0%; Pred. No. 8.6e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IQAVLSLYASGRRTG 15

Db 136 IQAVLSLYASGRRTG 150

RESULT 6

US-09-171-337A-7

; Sequence 7, Application US/09171337A

; Patent No. 6300095

GENERAL INFORMATION:

APPLICANT: BARREDO FUENTE, Jose Luis

RODRIGUEZ SAIZ, Marta

COLLADOS DE LA VIEJA, Alfonso J.

MORENO VALLE, Migueu Angel

SALTO MALDONADO, Francisco

DIEZ GARCIA, Bruno

TITLE OF INVENTION: PROMOTERS OF THE GENES GLUTAMATE

DESHYDROGENASE, -N-ACETYLHEXOSAMINIDASE

AND -ACTIN AND THEIR USE IN FILAMENTOUS

FUNGI EXPRESSION, SECRETION AND ANTISENSE

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: LADAS & PARRY

STREET: 26 WEST 61 STREET

CITY: NEW YORK

STATE: NY

COUNTRY: USA

ZIP: 10023

COMPUTER READABLE FORM:

MEDIUM TYPE: 3-1/4" Disk 1.44MB

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11

SOFTWARE: WordPerfect 8 for Windows

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/171,337A

FILING DATE: 14-May-1999

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/ES98/00056

FILING DATE: 5-MAR-1998

APPLICATION NUMBER: ES9700482

FILING DATE: 5-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: MASS, Clifford J.

REGISTRATION NUMBER: 30,086

TELECOMMUNICATION INFORMATION: (C) REF./DOCKET NO.: U-011948-3

TELEPHONE: 233288

INFORMATION FOR SEQ ID NO: 7

SEQUENCE CHARACTERISTICS:

LENGTH: 375 amino acids

TYPE: amino acids

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: Penicillium chrysogenum

FEATURE:

OTHER INFORMATION: amino acid sequence of the -actin

protein with a molecular weight of

41760 Da.

SEQUENCE DESCRIPTION: SEQ ID NO: 7

US-09-171-337A-7

Query Match 100.0%; Score 71; DB 3; Length 375;

Best Local Similarity 100.0%; Pred. No. 8.6e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IQAVLSLYASGRRTG 15

Db 136 IQAVLSLYASGRRTG 150

RESULT 7

US-09-171-337A-8

; Sequence 8, Application US/09171337A

; Patent No. 6300095

GENERAL INFORMATION:

APPLICANT: BARREDO FUENTE, Jose Luis

RODRIGUEZ SAIZ, Marta

COLLADOS DE LA VIEJA, Alfonso J.

MORENO VALLE, Migueu Angel

SALTO MALDONADO, Francisco

DIEZ GARCIA, Bruno

TITLE OF INVENTION: PROMOTERS OF THE GENES GLUTAMATE

DESHYDROGENASE, -N-ACETYLHEXOSAMINIDASE

AND -ACTIN AND THEIR USE IN FILAMENTOUS

FUNGI EXPRESSION, SECRETION AND ANTISENSE

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: LADAS & PARRY

STREET: 26 WEST 61 STREET

CITY: NEW YORK

STATE: NY

COUNTRY: USA

ZIP: 10023

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/631,022
FILING DATE: 02-AUG-2000
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/171,337
FILING DATE: 14-MAY-1999
APPLICATION NUMBER: PCT/ES98/00056
FILING DATE: 5-MAR-1998
APPLICATION NUMBER: ES9700482
FILING DATE: 5-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: MASS, Clifford J.
REGISTRATION NUMBER: 30,086
REGISTRATION NO.: U-02886-6

TELECOMMUNICATION INFORMATION:
TELEPHONE: 233288
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Penicillium chrysogenum
FEATURE:
OTHER INFORMATION: amino acid sequence of the -actin
protein with a molecular weight of
41760 Da.
SEQUENCE DESCRIPTION: SEQ ID NO: 7
US-09-631-022-7

Query Match 100.0%; Score 71; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 8.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRRTG 15
DB 136 IQAVLSLYASGRRTG 150

RESULT 9
US-09-631-022-8
; Sequence 8, Application US/09631022
; Patent No. 6558921
; GENERAL INFORMATION:
; APPLICANT: BARREDO FUENTE, Jose Luis
; RODRIGUEZ SAIZ, Marta
; COLLADOS DE LA VIEJA, Alfonso J.
; MORENO VALLE,Miguel Angel
; SALTO MALDONADO, Francisco
; DIEZ GARCIA, Bruno
; TITLE OF INVENTION: PROMOTERS OF THE GENES GLUTAMATE
DESHYDROGENASE, -N-ACETYLHEXOSAMINIDASE
AND -ACTIN AND THEIR USE IN FILAMENTOUS
FUNGI EXPRESSION, SECRETION AND ANTISENSE

NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: LADAS & PARRY
STREET: 26 WEST 61 STREET
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10023
COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/4" Disk 1.44MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11
SOFTWARE: WordPerfect 8 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/631,022
FILING DATE: 02-AUG-2000

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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
FILING DATE: 09/171,337
APPLICATION NUMBER: PCT/ES98/00056
FILING DATE: 14-MAY-1999
APPLICATION NUMBER: ES9700482
FILING DATE: 5-MAR-1998
APPLICATION NUMBER: ES9700482
FILING DATE: 5-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: MASS, Clifford J.
REGISTRATION NUMBER: 30,086
TELECOMMUNICATION INFORMATION:
(C) REF./DOCKET NO.: U-02886-6
TELEPHONE: 233288
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
ORIGINAL SOURCE:
ORGANISM: Acromonium chrysogenum
FEATURE:
OTHER INFORMATION: amino acid sequence of the -actin
protein with a molecular weight of
41612 Da.
SEQUENCE DESCRIPTION: SEQ ID NO: 8

US-09-631-022-8

Query Match 100.0%; Score 71; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 8.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRRTG 15
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DB 136 IQAVLSLYASGRRTG 150

RESULT 10

US-09-976-594-731
Sequence 731, Application US/09976594
Patent No. 6673549
GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
SEQ ID NO 731
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673549 1837317CD1
US-09-976-594-731

Query Match 100.0%; Score 71; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 8.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRRTG 15
|||||
DB 136 IQAVLSLYASGRRTG 150

RESULT 11

US-08-588-113-2
Sequence 2, Application US/08588113
Patent No. 5710003
GENERAL INFORMATION:
APPLICANT: McHugh, Kirk M.
TITLE OF INVENTION: DIAGNOSTIC TEST FOR DETERMINING
TITLE OF INVENTION: MALIGNANCY OF SMOOTH MUSCLE TUMORS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 571003ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,113
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Ralph, Rebecca L.
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: TUU-1652
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-588-113-2

Query Match 100.0%; Score 71; DB 1; Length 376;
Best Local Similarity 100.0%; Pred. No. 8.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRRTG 15
|||||
DB 137 IQAVLSLYASGRRTG 151

RESULT 12

US-09-949-016-6100
Sequence 6100, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6100
LENGTH: 376
TYPE: PRT
ORGANISM: Human
US-09-949-016-6100

Query Match 100.0%; Score 71; DB 4; Length 376;
Best Local Similarity 100.0%; Pred. No. 8.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IQAVLSLYASGRRTTG 15
Db 137 IQAVLSLYASGRRTTG 151

RESULT 13

US-09-106-217-2
; Sequence 2, Application US/09106217
; Patent No. 6063576
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Olson, Timothy M.
; TITLE OF INVENTION: Actin Mutations in Dilated
; TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESS: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; CITY: Tower
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,217
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 2323-125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-106-217-2
Query Match 100.0%; Score 71; DB 3; Length 377;
Best Local Similarity 100.0%; Pred. No. 8.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IQAVLSLYASGRRTTG 15
Db 138 IQAVLSLYASGRRTTG 152

RESULT 14

US-09-919-172-33
; Sequence 33, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469

Query Match 100.0%; Score 71; DB 3; Length 377;
Best Local Similarity 100.0%; Pred. No. 8.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IQAVLSLYASGRRTTG 15
Db 138 IQAVLSLYASGRRTTG 152

; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 33
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673545 1709118CDI
US-09-919-172-33

Query Match 100.0%; Score 71; DB 4; Length 377;
Best Local Similarity 100.0%; Pred. No. 8.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IQAVLSLYASGRRTTG 15
Db 138 IQAVLSLYASGRRTTG 152

RESULT 15

US-09-917-254-53
; Sequence 53, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
; APPLICANT: Mutter, George
; APPLICANT: Baak, Jan
; TITLE OF INVENTION: Prognostic Classification of Breast Cancer
; FILE REFERENCE: B0801/7224(JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/222,093
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 53
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-917-254-53

Query Match 100.0%; Score 71; DB 4; Length 377;
Best Local Similarity 100.0%; Pred. No. 8.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IQAVLSLYASGRRTTG 15
Db 138 IQAVLSLYASGRRTTG 152

Search completed: April 8, 2005, 12:07:38
Job time : 18.5333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 10:53:18 ; Search time 42.6667 seconds

(without alignments)
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Title: US-09-423-351C-10

Perfect score: 71

Sequence: 1 IQAVLSLYASGRITG 15

Scoring table: BLOSUM62

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Searched: 1418010 seqs, 331997259 residues

Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep:*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
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- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	71	100.0	97	US-09-864-761-33414	Sequence 33414, A
2	71	100.0	168	US-10-264-049-4044	Sequence 4044, Ap
3	71	100.0	180	US-10-437-963-169247	Sequence 169247, Ap
4	71	100.0	183	US-10-264-049-3432	Sequence 3432, Ap
5	71	100.0	197	US-10-424-599-280810	Sequence 280810, Ap
6	71	100.0	204	US-10-264-049-4148	Sequence 4148, Ap
7	71	100.0	208	US-10-424-599-282905	Sequence 282905, Ap
8	71	100.0	219	US-10-002-631C-56	Sequence 56, Appl
9	71	100.0	230	US-10-767-701-42770	Sequence 42770, A
10	71	100.0	236	US-10-424-599-206389	Sequence 206389, Ap
11	71	100.0	237	US-10-424-599-143226	Sequence 143226, Ap
12	71	100.0	248	US-10-424-599-162684	Sequence 162684, Ap
13	71	100.0	249	US-10-767-701-43575	Sequence 43575, A

Sequence 44494, A
Sequence 69353, A
Sequence 177530, A
Sequence 52089, A
Sequence 57500, A
Sequence 278431, A
Sequence 62158, A
Sequence 59172, A
Sequence 28333, A
Sequence 3002, Ap
Sequence 68, Appl
Sequence 93, Appl
Sequence 88, Appl
Sequence 2436, Ap
Sequence 5927, Ap
Sequence 94, Appl
Sequence 82, Appl
Sequence 101, Appl
Sequence 179917, A
Sequence 202420, A
Sequence 45677, A
Sequence 46090, A
Sequence 33, Appl
Sequence 52, Appl
Sequence 64, Appl
Sequence 162009, A
Sequence 162685, A
Sequence 162686, A
Sequence 22816, A
Sequence 223492, A
Sequence 283336, A
Sequence 66124, A

ALIGNMENTS

RESULT 1

US-09-864-761-33414
; Sequence 33414, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33414
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006483.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 18
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 48
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 81
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 28
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 24
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 85
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 78
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 37
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 45
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 40
; OTHER INFORMATION: EST HUMAN HIT: BE271730.1, EVALUATE 3.00e-50
; OTHER INFORMATION: SWISSPROT HIT: Q42161, EVALUATE 4.00e-51
; OTHER INFORMATION: EST HUMAN HIT: BE256272.1, EVALUATE 4.00e-50
US-09-864-761-33414

Query Match 100.0%; Score 71; DB 9; Length 97;
Best Local Similarity 100.0%; Pred. No. 8.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRRTG 15
Db 15 IQAVLSLYASGRRTG 29

RESULT 2
US-10-264-049-4044
; Sequence 4044, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4044
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-4044

Query Match 100.0%; Score 71; DB 15; Length 168;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRRTG 15
Db 15 IQAVLSLYASGRRTG 15

US-10-437-963-169247
; Sequence 169247, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 169247
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_67685C.1.pep
US-10-437-963-169247

Query Match 100.0%; Score 71; DB 16; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRRTG 15
Db 71 IQAVLSLYASGRRTG 85

RESULT 4
US-10-264-049-3432
; Sequence 3432, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 3432
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (4)_FEATURE
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (11)_FEATURE
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (12)_FEATURE
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
```



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; NAME/KEY: MISC_FEATURE
; LOCATION: (13)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (22)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (33)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (83)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (89)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (113)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (117)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (136)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (149)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (161)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (172)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (174)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
;
US-10-264-049-3432

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Query Match      100.0%; Score 71; DB 15; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 IQAVLSLYASGRRTTG 15
Db 44 IQAVLSLYASGRRTTG 58

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```

RESULT 5
US-10-424-599-280810
; Sequence 280810, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684

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```

; SEQ ID NO 280810
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(197)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_95594C.1.pap
US-10-424-599-280810

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Query Match      100.0%; Score 71; DB 15; Length 197;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 IQAVLSLYASGRRTTG 15
Db 138 IQAVLSLYASGRRTTG 152

```

```

RESULT 6
US-10-264-049-4148
; Sequence 4148, Application US/10264049
; Publication No. US2004000579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133PI
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4148
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-4148

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Query Match      100.0%; Score 71; DB 15; Length 204;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 IQAVLSLYASGRRTTG 15
Db 156 IQAVLSLYASGRRTTG 170

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RESULT 7
US-10-424-599-282905
; Sequence 282905, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 282905
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure

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; LOCATION: (1)...(208)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_97486C.1.pep
US-10-424-599-282905

Query Match      100.0%; Score 71; DB 15; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRRTG 15
    |||||
Db 138 IQAVLSLYASGRRTG 152

RESULT 8
US-10-002-631C-56
; Sequence 56, Application US/10002631C
; Publication No. US20030157486A1
; GENERAL INFORMATION:
; APPLICANT: Muenster, Matthew
; TITLE OF INVENTION: METHODS TO IDENTIFY SIGNAL SEQUENCES
; FILE REFERENCE: A34943 090495.0243
; CURRENT APPLICATION NUMBER: US/10/002,631C
; PRIOR FILING DATE: 2001-10-31
; CURRENT APPLICATION NUMBER: 60/300,309
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-631C-56

Query Match      100.0%; Score 71; DB 14; Length 219;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRRTG 15
    |||||
Db 163 IQAVLSLYASGRRTG 177

RESULT 9
US-10-767-701-42770
; Sequence 42770, Application US/10767701
; Publication No. US20040172694A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53235)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 42770
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CI7410_1.pep
US-10-767-701-42770

Query Match      100.0%; Score 71; DB 16; Length 230;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRRTG 15
    |||||
Db 1 IQAVLSLYASGRRTG 152

RESULT 10
US-10-424-599-206389
; Sequence 206389, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 206389
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(236)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_28396C.1.pep
US-10-424-599-206389

Query Match      100.0%; Score 71; DB 15; Length 236;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRRTG 15
    |||||
Db 6 IQAVLSLYASGRRTG 20

RESULT 11
US-10-424-599-143226
; Sequence 143226, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 143226
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(237)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_100347C.1.pep
US-10-424-599-143226

Query Match      100.0%; Score 71; DB 15; Length 237;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IQAVLSLYASGRRTG 15
    |||||
Db 20 IQAVLSLYASGRRTG 34
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RESULT 12
US-10-424-599-162684
; Sequence 162684, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 162684
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_117922C.1.pep
US-10-424-599-162684

Query Match 100.0%; Score 71; DB 15; Length 248;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IQAVLSLYASGRRTG 15
| | | | | | | | | | | | | | | | | | | | | |
Db 138 IQAVLSLYASGRRTG 152

RESULT 13
US-10-767-701-43575
; Sequence 43575, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 43575
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C5949_1.pep
US-10-767-701-43575

Query Match 100.0%; Score 71; DB 16; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IQAVLSLYASGRRTG 15
| | | | | | | | | | | | | | | | | | | | | |
Db 10 IQAVLSLYASGRRTG 24

RESULT 14
US-10-425-114-44494
; Sequence 44494, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 44494
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700978095_FLI.pep
US-10-425-114-44494

Query Match 100.0%; Score 71; DB 15; Length 250;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IQAVLSLYASGRRTG 15
| | | | | | | | | | | | | | | | | | | | | |
Db 11 IQAVLSLYASGRRTG 25

RESULT 15
US-10-425-114-69353
; Sequence 69353, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 69353
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73022E07_FLI.pep
US-10-425-114-69353

Query Match 100.0%; Score 71; DB 15; Length 254;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IQAVLSLYASGRRTG 15
| | | | | | | | | | | | | | | | | | | | | |
Db 15 IQAVLSLYASGRRTG 29

Search completed: April 8, 2005, 12:51:00
Job time : 42.6667 secs

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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:57 ; Search time 17.5333 Seconds
(without alignments)
63.863 Million cell updates/sec

Title: US-09-423-351C-9
Perfect score: 76
Sequence: 1 DEAQSKRGILTLPYP 15

Scoring table: BLOSUM62
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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	100.0	80	3	US-09-306-446C-4
2	76	100.0	374	3	US-08-609-236-6
3	76	100.0	374	3	US-09-306-446C-2
4	76	100.0	375	2	US-08-494-151-14
5	76	100.0	375	3	US-09-106-217-16
6	76	100.0	375	4	US-09-978-594-731
7	76	100.0	376	1	US-08-588-113-2
8	76	100.0	376	4	US-09-949-016-6100
9	76	100.0	377	3	US-09-106-217-2
10	76	100.0	377	4	US-09-919-172-33
11	76	100.0	377	4	US-09-917-254-53
12	76	100.0	386	4	US-09-949-016-7721
13	76	100.0	399	4	US-09-949-016-9424
14	76	100.0	402	4	US-09-949-016-10757
15	76	100.0	404	4	US-09-949-016-11313
16	73	96.1	371	1	US-08-261-206A-77
17	73	96.1	375	3	US-09-171-337A-7
18	73	96.1	375	3	US-09-171-337A-8
19	73	96.1	375	4	US-09-631-022-8
20	73	96.1	375	4	US-09-631-022-8
21	73	96.1	377	4	US-09-248-796A-14109
22	56	73.7	91	4	US-09-621-978-6520
23	46	60.5	376	4	US-09-538-092-1110
24	46	60.5	376	4	US-09-949-016-6656
25	46	60.5	376	4	US-09-949-016-8452
26	44	57.9	384	4	US-09-538-092-395
27	42	55.3	147	4	US-09-902-540-12005

28	42	55.3	362	4	US-09-949-016-7725	Sequence 7725, Ap
29	40	52.6	376	4	US-09-538-092-1109	Sequence 1109, Ap
30	40	52.6	496	4	US-09-248-796A-19404	Sequence 19404, A
31	39	51.3	247	4	US-09-171-337C-11	Sequence 11, Appl
32	39	51.3	266	3	US-09-134-001C-4962	Sequence 4962, Ap
33	39	51.3	333	4	US-09-107-532A-4886	Sequence 4886, Ap
34	38	50.0	391	4	US-09-543-681A-8292	Sequence 8292, Ap
35	37	48.7	131	4	US-09-902-540-11500	Sequence 11500, A
36	37	48.7	226	4	US-09-107-532A-5362	Sequence 5362, Ap
37	37	48.7	394	4	US-09-949-016-6655	Sequence 6655, Ap
38	37	48.7	406	4	US-09-949-016-7396	Sequence 7396, Ap
39	37	48.7	417	4	US-09-328-352-4772	Sequence 4772, Ap
40	37	48.7	1382	3	US-09-057-570-4	Sequence 4, Appl
41	37	48.7	1382	4	US-09-387-693-4	Sequence 4, Appl
42	37	48.7	1867	4	US-09-824-574-5	Sequence 5, Appl
43	36	47.4	101	4	US-09-732-210-755	Sequence 755, App
44	36	47.4	254	4	US-09-631-594-67	Sequence 67, Appl
45	36	47.4	432	2	US-08-472-172-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-306-446C-4
; Sequence 4, Application US/09306446C
; Patent No. 6372959
; GENERAL INFORMATION:
; APPLICANT: KIM, Dong Soo
; APPLICANT: KIM, Chul Geun
; APPLICANT: NAM, Yoon Kwon
; APPLICANT: NOH, Jae Koo
; APPLICANT: CHO, Kyou Nam
; TITLE OF INVENTION: EXPRESSION VECTOR OF MUD LOACH GROWTH HORMONE GENE
; FILE REFERENCE: P06344050/BAS
; CURRENT APPLICATION NUMBER: US/09/306.446C
; CURRENT FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: KR 98/20255
; PRIOR FILING DATE: 1998-06-01
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 4
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Misgurnus mizolepus
US-09-306-446C-4

Query Match 100.0%; Score 76; DB 3; Length 80;
Best Local Similarity 100.0%; Pred. No. 4.8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLPYP 15
Db 15 DEAQSKRGILTLPYP 29

RESULT 2
US-08-609-236-6
; Sequence 6, Application US/08609236
; Patent No. 6087398
; GENERAL INFORMATION:
; APPLICANT: Steven R. Goodman
; TITLE OF INVENTION: No. 6087398el Sickle Cell Anemia Treatment
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McGregor & Adler, LLP
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,236
FILING DATE: March 1, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/002,288
FILING DATE: August 14, 1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5807
TELEPHONE: 713-777-2321
TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 374
TYPE: Amino acid
STRANDEDNESS:
TOPOLOGY: Linear
MOLECULE TYPE: Protein
DESCRIPTION: No
HYPOTHETICAL: No
ANTI-SENSE: No
FRAGMENT TYPE:
ORIGINAL SOURCE:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
US-08-609-236-6

Query Match 100.0%; Score 76; DB 3; Length 374;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLYKYP 15
Db 55 DEAQSKRGILTLYKYP 69

RESULT 3
US-09-306-446C-2
Sequence 2, Application US/09306446C
Patent No. 6372959
GENERAL INFORMATION:
APPLICANT: KIM, Dong Soo
APPLICANT: KIM, Chul Geun
APPLICANT: NAM, Yoon Kwon
APPLICANT: NOH, Jae Koo
APPLICANT: CHO, Kyou Nam
TITLE OF INVENTION: EXPRESSION VECTOR OF MUD LOACH GROWTH HORMONE GENE
FILE REFERENCE: P06344USO/BAS
CURRENT APPLICATION NUMBER: US/09/306,446C
CURRENT FILING DATE: 1999-05-06
PRIOR APPLICATION NUMBER: KR 98/20255
PRIOR FILING DATE: 1998-06-01
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 374
TYPE: PRT
ORGANISM: Misgurnus mizolepus
US-09-306-446C-2

Query Match 100.0%; Score 76; DB 3; Length 374;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DEAQSKRGILTLYKYP 15
Db 56 DEAQSKRGILTLYKYP 70
RESULT 4
US-08-494-151-14
Sequence 14, Application US/08494151
Patent No. 5840528
GENERAL INFORMATION:
APPLICANT: Van Ooyen, Albert Johannes Joseph
TITLE OF INVENTION: Transformation of Phaffia rhodozyma
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,151
FILING DATE: 23-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20039.01
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-494-151-14

Query Match 100.0%; Score 76; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLYKYP 15
Db 56 DEAQSKRGILTLYKYP 70

RESULT 5
US-09-106-217-16
Sequence 16, Application US/09106217
Patent No. 6063576
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Olson, Timothy M.
TITLE OF INVENTION: Actin Mutations in Dilated
TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
STREET: 555 Thirteenth Street, N.W., Suite 701 East
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/09/106,217
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 2323-125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-783-6040
TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-106-217-16

Query Match 100.0%; Score 76; DB 3; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLYKYP 15
|||||
Db 56 DEAQSKRGILTLYKYP 70

RESULT 6

US-09-976-594-731
Sequence 731, Application US/09976594
Patent No. 6673549
GENERAL INFORMATION:
APPLICANT: Furness, Michael

APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
SEQ ID NO 731
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673549 1837317CD1
US-09-976-594-731

Query Match 100.0%; Score 76; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLYKYP 15
|||||
Db 56 DEAQSKRGILTLYKYP 70

RESULT 7

US-08-588-113-2
Sequence 2, Application US/08588113
Patent No. 5710003
GENERAL INFORMATION:
APPLICANT: McHugh, Kirk M.
TITLE OF INVENTION: DIAGNOSTIC TEST FOR DETERMINING

TITLE OF INVENTION: MALIGNANCY OF SMOOTH MUSCLE TUMORS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 5710003ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/588,113
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Ralph, Rebecca L.
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: TJU-1652
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-588-113-2

Query Match 100.0%; Score 76; DB 1; Length 376;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLYKYP 15
|||||
Db 57 DEAQSKRGILTLYKYP 71

RESULT 8

US-09-949-016-6100
Sequence 6100, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6100
LENGTH: 376
TYPE: PRT
ORGANISM: Human
US-09-949-016-6100

Query Match 100.0%; Score 76; DB 4; Length 376;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLYKYP 15

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Db      57 DEAQSKRGILTLYKYP 71
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RESULT 9
US-09-106-217-2
; Sequence 2, Application US/09106217
; Patent No. 6063576
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; TITLE OF INVENTION: Actin Mutations in Dilated
; TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; STREET: Tower
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,217
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 2323-125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-106-217-2

Query Match      100.0%; Score 76; DB 3; Length 377;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DEAQSKRGILTLYKYP 15
|||||
DB      58 DEAQSKRGILTLYKYP 72
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RESULT 10
US-09-919-172-33
; Sequence 33, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Faria, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 33
; LENGTH: 377
; TYPE: PRT
US-09-919-172-33

Query Match      100.0%; Score 76; DB 4; Length 386;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 1709118CDI
US-09-919-172-33

Query Match      100.0%; Score 76; DB 4; Length 377;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DEAQSKRGILTLYKYP 15
|||||
DB      58 DEAQSKRGILTLYKYP 72
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RESULT 11
US-09-917-254-53
; Sequence 53, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
; APPLICANT: Mutter, George
; APPLICANT: Baak, Jan
; TITLE OF INVENTION: Prognostic Classification of Breast Cancer
; FILE REFERENCE: B0801/7224(JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/222,093
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 53
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-917-254-53

Query Match      100.0%; Score 76; DB 4; Length 377;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DEAQSKRGILTLYKYP 15
|||||
DB      58 DEAQSKRGILTLYKYP 72
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RESULT 12
US-09-949-016-7721
; Sequence 7721, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7721
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7721

Query Match      100.0%; Score 76; DB 4; Length 386;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 DEAQSKRGILTLYP 15
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Db 67 DEAQSKRGILTLYP 81

RESULT 13
US-09-949-016-9424
; Sequence 9424, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9424
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9424

Query Match 100.0%; Score 76; DB 4; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLYP 15
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Db 80 DEAQSKRGILTLYP 94

RESULT 14
US-09-949-016-10757
; Sequence 10757, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10757
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10757

Query Match 100.0%; Score 76; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLYP 15
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Db 83 DEAQSKRGILTLYP 97

RESULT 15
US-09-949-016-11313
; Sequence 11313, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11313
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11313

Query Match 100.0%; Score 76; DB 4; Length 404;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLYP 15
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Db 85 DEAQSKRGILTLYP 99

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Title: US-09-423-351C-9
Perfect score: 76
Sequence: 1 DEAQSKRGILTLLKY

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Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 su

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2	76	100.0	108	9	US-09-864-761-37942	Sequence 37942, A
3	76	100.0	135	16	US-10-767-701-47318	Sequence 47318, A
4	76	100.0	136	15	US-10-424-599-280811	Sequence 280811, A
5	76	100.0	142	15	US-10-424-599-184471	Sequence 184471, A
6	76	100.0	197	15	US-10-424-599-280810	Sequence 280810, A
7	76	100.0	201	15	US-10-264-049-4308	Sequence 4308, A
8	76	100.0	204	15	US-10-264-049-4148	Sequence 4148, A
9	76	100.0	208	15	US-10-424-599-282905	Sequence 282905, A
10	76	100.0	219	14	US-10-002-631C-56	Sequence 56, App
11	76	100.0	219	14	US-10-029-386-32056	Sequence 32056, App
12	76	100.0	230	16	US-10-767-701-42770	Sequence 42770, A
13	76	100.0	248	15	US-10-424-599-162684	Sequence 162684, A

14	76	100.0	331	15	US-10-425-114-59172	Sequence 59172, A
15	76	100.0	342	15	US-10-108-260A-4008	Sequence 4008, Ap
16	76	100.0	347	15	US-10-424-599-28333	Sequence 28333, A
17	76	100.0	371	16	US-10-322-281-68	Sequence 68, Appl
18	76	100.0	375	14	US-10-205-194-93	Sequence 93, Appl
19	76	100.0	375	14	US-10-316-253-88	Sequence 88, Appl
20	76	100.0	375	15	US-10-369-493-2436	Sequence 2436, Ap
21	76	100.0	375	15	US-10-369-493-5927	Sequence 5927, Ap
22	76	100.0	375	15	US-10-205-331-94	Sequence 94, Appl
23	76	100.0	375	15	US-10-260-708-82	Sequence 82, Appl
24	76	100.0	376	15	US-10-341-434-101	Sequence 101, App
25	76	100.0	376	16	US-10-437-963-203420	Sequence 202420, A
26	76	100.0	376	16	US-10-767-701-45677	Sequence 45677, A
27	76	100.0	377	9	US-09-919-172-33	Sequence 33, Appl
28	76	100.0	377	14	US-10-238-777-52	Sequence 52, Appl
29	76	100.0	377	15	US-10-336-031B-64	Sequence 64, Appl
30	76	100.0	377	15	US-10-424-599-162009	Sequence 162009, A
31	76	100.0	377	15	US-10-424-599-163685	Sequence 163685, A
32	76	100.0	377	15	US-10-424-599-162686	Sequence 162686, A
33	76	100.0	377	15	US-10-424-599-222816	Sequence 222816, A
34	76	100.0	377	15	US-10-424-599-223492	Sequence 223492, A
35	76	100.0	377	15	US-10-424-599-283336	Sequence 283336, A
36	76	100.0	377	15	US-10-425-114-66124	Sequence 66124, A
37	76	100.0	377	16	US-10-333-680-4	Sequence 4, Appl
38	76	100.0	377	16	US-10-437-963-121952	Sequence 121952, A
39	76	100.0	377	16	US-10-437-963-148877	Sequence 148877, A
40	76	100.0	377	16	US-10-437-963-198295	Sequence 198295, A
41	76	100.0	377	16	US-10-767-701-47239	Sequence 47239, A
42	76	100.0	378	15	US-10-425-114-42317	Sequence 42317, A
43	76	100.0	378	15	US-10-425-114-52458	Sequence 52458, A
44	76	100.0	378	15	US-10-425-114-59365	Sequence 59365, A
45	76	100.0	378	15	US-10-425-114-59367	Sequence 59367, A

ALIGNMENTS

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RESULT 1
US-10-264-049-3601
; Sequence 3601, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133PI
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 3601
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (103)
; OTHER INFORMATION: Xaa equals any of the twenty naturally
US-10-264-049-3601

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Query Match      100.0%; Score 76; DB 15; Length 105;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DEAQSRGILTLKYP 15
        ||| ||||| ||||| |||
Db      57 DEAQSRGILTLKYP 71

RESULT 2

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US-09-864-761-37942
; Sequence 37942, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR FILING DATE: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 37942
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC012271.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 14
; OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 17
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 62
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 13
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 28
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 9.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 27
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 14
; OTHER INFORMATION: SWISSPROT HIT: O15998, EVALUE 9.00e-60
; OTHER INFORMATION: EST_HUMAN HIT: BF127509.1, EVALUE 2.00e-58
US-09-864-761-37942
Query Match 100.0%; Score 76; DB 9; Length 108;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DEAQSKRGILTLYP 15
Db 15 DEAQSKRGILTLYP 29
RESULT 3
US-10-767-701-47318
; Sequence 47318, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 47318
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(135)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C105_2.pep
US-10-767-701-47318
Query Match 100.0%; Score 76; DB 16; Length 135;
Best Local Similarity 100.0%; Pred. No. 6.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DEAQSKRGILTLYP 15
Db 58 DEAQSKRGILTLYP 72
RESULT 4
US-10-424-599-280811
; Sequence 280811, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 280811
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_95595C.1.pep
US-10-424-599-280811
Query Match 100.0%; Score 76; DB 15; Length 136;
Best Local Similarity 100.0%; Pred. No. 6.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DEAQSKRGILTLYP 15
Db 58 DEAQSKRGILTLYP 72

RESULT 5
US-10-424-599-184471
; Sequence 184471, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 184471
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_137594C.1.pap
US-10-424-599-184471

Query Match 100.0%; Score 76; DB 15; Length 142;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLYKYP 15
|||||
Db 65 DEAQSKRGILTLYKYP 79

RESULT 6
US-10-424-599-280810
; Sequence 280810, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 280810
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(197)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_95594C.1.pap
US-10-424-599-280810

Query Match 100.0%; Score 76; DB 15; Length 197;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLYKYP 15
|||||
Db 58 DEAQSKRGILTLYKYP 72

RESULT 7
US-10-264-049-4308
; Sequence 4308, Application US/10264049
; Publication No. US20040005579A1

; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4308
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (135)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (136)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (140)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (143)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (144)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (145)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (151)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (159)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (172)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (174)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (180)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; US-10-264-049-4308

Query Match 100.0%; Score 76; DB 15; Length 201;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLYKYP 15
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Db 73 DEAQSKRGILTLYKYP 87

RESULT 8
US-10-264-049-4148

; Sequence 4148, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133PI
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCR/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4148
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-4148

Query Match 100.0%; Score 76; DB 15; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLYKYP 15
|||||
Db 76 DEAQSKRGILTLYKYP 90
|||||

RESULT 9

US-10-424-599-282905
; Sequence 282905, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 282905
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Glycine max
; NAME/KEY: unsure
; LOCATION: (1)-(208)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_97486C.1.pep
US-10-424-599-282905

Query Match 100.0%; Score 76; DB 15; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLYKYP 15
|||||
Db 58 DEAQSKRGILTLYKYP 72
|||||

RESULT 10

US-10-002-631C-56
; Sequence 56, Application US/10002631C
; Publication No. US20030157486A1
; GENERAL INFORMATION:
; APPLICANT: Graff, Jonathon M.
; APPLICANT: Muenster, Matthew
; TITLE OF INVENTION: METHODS TO IDENTIFY SIGNAL SEQUENCES

; FILE REFERENCE: A34943 090495.0243
; CURRENT APPLICATION NUMBER: US/10/002,631C
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/300,309
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-631C-56

Query Match 100.0%; Score 76; DB 14; Length 219;
Best Local Similarity 100.0%; Pred. No. 1.e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLYKYP 15
|||||
Db 83 DEAQSKRGILTLYKYP 97
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RESULT 11

US-10-029-386-32056
; Sequence 32056, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: ASOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32056
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC026717.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 16
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 23
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 6.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 20
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9.8
; OTHER INFORMATION: SWISSPROT HIT: P29751, EVALUATION 3.00e-94
US-10-029-386-32056

Query Match 100.0%; Score 76; DB 14; Length 219;
Best Local Similarity 100.0%; Pred. No. 1.e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTLYKYP 15
|||||
Db 87 DEAQSKRGILTLYKYP 101
|||||

RESULT 12

US-10-767-701-42770
; Sequence 42770, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29

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; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 42770
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28WY03-C17410_1.pep
US-10-767-701-42770

Query Match      100.0%; Score 76; DB 16; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DEAQSKRGILTLYP 15
Db      58 DEAQSKRGILTLYP 72

RESULT 13
US-10-424-599-162684
; Sequence 162684, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424.599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 162684
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_117922C.1.pep
US-10-424-599-162684

Query Match      100.0%; Score 76; DB 15; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DEAQSKRGILTLYP 15
Db      58 DEAQSKRGILTLYP 72

RESULT 14
US-10-425-114-59172
; Sequence 59172, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425.114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 59172
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700332871_FLI.pep
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US-10-425-114-59172

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Query Match      100.0%; Score 76; DB 15; Length 331;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 DEAQSKRGILTLYP 15
Db      12 DEAQSKRGILTLYP 26
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RESULT 15
US-10-108-260A-4008
; Sequence 4008, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108.260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4008
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-4008
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Query Match      100.0%; Score 76; DB 15; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 DEAQSKRGILTLYP 15
Db      58 DEAQSKRGILTLYP 72
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Search completed: April 8, 2005, 12:51:00
Job time : 42.6667 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 9.33333 Seconds
(without alignments)
154.634 Million cell updates/sec

Title: US-09-423-351C-8

Perfect score: 75

Sequence: 1 LASLSTFQQMWSKQ 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	100.0	42	JE0005	actin alpha, smoot
2	75	100.0	100	S14851	actin - fruit fly
3	75	100.0	137	A28258	actin 5C - fruit f
4	75	100.0	195	S39777	actin beta - pig (
5	75	100.0	213	A61043	actin CAL5 - sea s
6	75	100.0	308	A03000	actin 3 - fruit fl
7	75	100.0	327	S11452	actin (clone 302)
8	75	100.0	349	B25819	actin, fetal skele
9	75	100.0	370	A29664	actin - sea urchin
10	75	100.0	374	ATBOB	actin beta - bovin
11	75	100.0	374	ATBOG	actin gamma - bovi
12	75	100.0	374	JC5818	gamma-actin - huma
13	75	100.0	375	ATBOSM	actin, aortic smoo
14	75	100.0	375	ATRTC	actin beta - rat
15	75	100.0	375	A48324	actin beta, cytosk
16	75	100.0	375	ATCHB	actin beta - chick
17	75	100.0	375	ATHUB	actin beta - human
18	75	100.0	375	ATHUG	actin gamma 1 - hu
19	75	100.0	375	ATMSB	actin beta - mouse
20	75	100.0	375	ATMSG	actin gamma - mous
21	75	100.0	375	ATRBB	actin beta, non-mu
22	75	100.0	375	S11222	actin gamma, cytos
23	75	100.0	375	S33386	actin, cytosolic (
24	75	100.0	375	JT0385	actin gamma - Emer
25	75	100.0	375	S47897	actin 1 - Pneumocy
26	75	100.0	375	T25272	hypothetical prote
27	75	100.0	375	A26836	actin - fission ye
28	75	100.0	375	S71125	actin beta-2, cyto
29	75	100.0	375	S71124	actin beta-1, cyto

actin beta, cytosol
actin beta - goose
actin alpha, cardi
actin - Puccinia g
actin 7 - fruit fl
actin gamma, cytos
actin 8 - fruit fl
actin Cyl - sea ur
Actin-1A - nematod
actin 87E - fruit
actin - fruit fly
actin, cytosolic -
actin, muscle - at
actin 15A - sea ur
actin - sea urchin
actin - Hydra atte

ALIGNMENTS

RESULT 1

JE0005

actin alpha, smooth muscle - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004

C:Accession: JE0005

R:Hsu, C.Y.J.; Frankel, F.R.

Gene 69, 345-348, 1988

A:Title: Conserved and unique sequences in the 3'-untranslated region of rat smooth-mus.

A:Reference number: JE0005; MUID:89172079; PMID:3234770

A:Accession: JE0005

A:Molecule type: mRNA

A:Residues: 1-42 <HSU>

A:Cross-references: UNIPROT:P70476; GB:M22757; NID:949983; PIDN:AAA74457.1; PID:G959539

C:Genetics:

A:Gene: sma

C:Superfamily: actin

C:Keywords: muscle; smooth muscle

Query Match 100.0%; Score 75; DB 2; Length 42;

Best Local Similarity 100.0%; Pred. No. 2.3e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFQQMWSKQ 15

Db 13 LASLSTFQQMWSKQ 27

RESULT 2

S14851

actin - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C:Accession: S14851

R:Burn, T.C.; Tobin, S.L.

submitted to the EMBL Data Library, October 1990

A:Reference number: S14851

A:Accession: S14851

A:Molecule type: DNA

A:Residues: 1-100 <BUR>

A:Cross-references: UNIPROT:P02572; EMBL:X54848; NID:g7549; PIDN:CAA38618.1; PID:g7550

C:Genetics:

A:Gene: FlyBase:Act42A

A:Cross-references: FlyBase:FBgn0000043

C:Superfamily: actin

C:Keywords: cell motility; cytoskeleton; microfilament; mitosis; structural protein

Query Match 100.0%; Score 75; DB 2; Length 100;

Best Local Similarity 100.0%; Pred. No. 5.6e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFQQMWSKQ 15

```

Db          71 LASLSTFQQMWSKQ 85
|||||
RESULT 3
A28258
actin 5C - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C:Accession: A28258
R:Vigoreaux, J.O.; Tobin, S.L.
Genes Dev. 1, 1161-1171, 1987
A:Title: Stage-specific selection of alternative transcriptional initiation sites from
A:Reference number: A28258; MUID:88112795; PMID:312314
A:Accession: A28258
A:Molecule type: mRNA
A:Residues: 1-137 <VIG>
A:Cross-references: UNIPROT:P10987
A:Note: the authors translated the codon GAG for residue 96 as Gly
C:Genetics:
A:Gene: FlyBase:Act5C
A:Cross-references: FlyBase:FBgn0000042
C:Superfamily: actin
C:Keywords: methylated amino acid
F:74/Modified site: 3'-methylhistidine (His) #status predicted

Query Match          100.0%; Score 75; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 7.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 LASLSTFQQMWSKQ 15
|||||
Db          108 LASLSTFQQMWSKQ 122
|||||
RESULT 4
S39777
actin beta - pig (fragments)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C:Accession: S39777
R:Adamski, J.; Husen, B.; Thole, H.H.; Groeschel-Stewart, U.; Jungblut, P.W.
Biochem. J. 296, 797-802, 1993
A:Title: Linkage of 17-beta-estradiol dehydrogenase to actin by epsilon-(gamma-glutamyl)
A:Reference number: S39777; MUID:94107247; PMID:8280079
A:Accession: S39777
A:Molecule type: protein
A:Residues: 1-20;21-52;53-79;80-85;86-95;96-116;117-151;152-159;160-195 <ADA>
A:Cross-references: UNIPROT:Q7M3B0
C:Superfamily: actin

Query Match          100.0%; Score 75; DB 2; Length 195;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 LASLSTFQQMWSKQ 15
|||||
Db          168 LASLSTFQQMWSKQ 182
|||||
RESULT 5
A61043
actin Cn15 - sea squirt (Styela clava) (fragments)
C:Species: Styela clava
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: A61043
R:Beach, R.L.; Jeffery, W.R.
Dev. Genet. 11, 2-14, 1990
A:Title: Temporal and spatial expression of a cytoskeletal actin gene in the ascidian
A:Reference number: A61043; MUID:90298580; PMID:2361333
A:Accession: A61043
A:Status: not compared with conceptual translation
A:Molecule type: mRNA

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A:Residues: 1-213 <BEA>
A:Cross-references: UNIPROT:Q7M3Y7
C:Comment: This sequence is expressed in cells undergoing rapid cell division.
C:Superfamily: actin
C:Keywords: cytoskeleton; methylated amino acid; mitosis; structural protein
F:73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match          100.0%; Score 75; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 LASLSTFQQMWSKQ 15
|||||
Db          184 LASLSTFQQMWSKQ 198
|||||
RESULT 6
A03000
actin 3 - fruit fly (Drosophila melanogaster) (fragments)
C:Species: Drosophila melanogaster
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: A03000
R:Fyrberg, B.A.; Bond, B.J.; Hershey, N.D.; Mixter, K.S.; Davidson, N.
Cell 24, 107-116, 1981
A:Title: The actin genes of Drosophila: protein coding regions are highly conserved but
A:Reference number: A03000; MUID:81210174; PMID:6263481
A:Accession: A03000
A:Molecule type: DNA
A:Residues: 1-308 <FYR>
A:Cross-references: UNIPROT:P02572
A:Note: there are 68 unsequenced residues between positions 160 and 161. Partial sequence
C:Genetics:
A:Gene: FlyBase:Act42A
A:Cross-references: FlyBase:FBgn0000043
A:Map position: 42A
C:Superfamily: actin
C:Keywords: methylated amino acid
F:74/Modified site: 3'-methylhistidine (His) #status predicted

Query Match          100.0%; Score 75; DB 2; Length 308;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 LASLSTFQQMWSKQ 15
|||||
Db          279 LASLSTFQQMWSKQ 293
|||||
RESULT 7
S11452
actin (clone 302) - brine shrimp (fragment)
C:Species: Artemia sp. (brine shrimp)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: S11452
R:Macias, M.T.; Sastre, L.
Nucleic Acids Res. 18, 5219-5225, 1990
A:Title: Molecular cloning and expression of four actin isoforms during Artemia developm
A:Reference number: S11450; MUID:90384823; PMID:2402445
A:Accession: S11452
A:Molecule type: mRNA
A:Residues: 1-327 <MAC>
A:Cross-references: UNIPROT:P18602; EMBL:X52604; NID:g5666; PIDN:CAA36837.1; PID:g829162
C:Superfamily: actin
C:Keywords: methylated amino acid; structural protein
F:25/Modified site: 3'-methylhistidine (His) #status predicted

Query Match          100.0%; Score 75; DB 2; Length 327;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 LASLSTFQQMWSKQ 15
|||||

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Db 298 LASLSTFQOMWISKQ 312

RESULT 8

B25819
actin, fetal skeletal/adult cardiac muscle - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 09-Jul-2004
C:Accession: B25819
R:Alonso, S.; Minty, A.; Bourlet, Y.; Buckingham, M.
J. Mol. Evol. 23, 11-22, 1986
A>Title: Comparison of three actin-coding sequences in the mouse; evolutionary relations
A:Reference number: A25819; MUID:86200234; PMID:3084797
A:Accession: B25819
A:Molecule type: mRNA
A:Residues: 1-349 <ALO>
A:Cross-references: UNIPROT:061275; GB:X03767; GB:J00381; GB:M10652; NID:G49869; PIDN:CA
C:Superfamily: actin
C:Keywords: cardiac muscle; heart; methylated amino acid; muscle; skeletal muscle
F:47/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 75; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFQOMWISKQ 15

Db 320 LASLSTFQOMWISKQ 334

RESULT 9

A29664
actin - sea urchin (Strongylocentrotus purpuratus)
C:Species: Strongylocentrotus purpuratus (purple urchin)
C>Date: 15-Dec-1988 #sequence_revision 30-Sep-1991 #text_change 05-Dec-1997
C:Accession: A29664
R:Crain Jr., W.R.; Boshar, M.F.; Cooper, A.D.; Durica, D.S.; Nagy, A.; Steffen, D.
J. Mol. Evol. 25, 37-45, 1987
A>Title: The sequence of a sea urchin muscle actin gene suggests a gene conversion with
A:Reference number: A29664; MUID:87311761; PMID:3114500
A:Accession: A29664
A:Molecule type: DNA
A:Residues: 1-370 <CRA>
A:Cross-references: GB:X05740; GB:X05741; GB:X05742; GB:X05743
A:Note: the authors translated the codon CAG for residue 260 as Glu
C:Superfamily: actin
C:Keywords: methylated amino acid
F:72/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 75; DB 2; Length 370;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFQOMWISKQ 15

Db 343 LASLSTFQOMWISKQ 357

RESULT 10

ATBOG
actin beta - bovine (tentative sequence)
C:Species: Bos primigenius taurus (cattle)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: E14185; A39105; A02999; A14185
R:Vandekerckhove, J.; Weber, K.
Eur. J. Biochem. 90, 451-462, 1978
A>Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain
A:Reference number: A14185; MUID:79045349; PMID:213279
A:Accession: E14185
A:Molecule type: protein
A:Residues: 1-374 <VAN>
A:Cross-references: UNIPROT:P60712
A:Note: only peptides that differed in composition from the corresponding peptides of ra

R;Degen, J.L.; Neubauer, M.G.; Degen, S.J.F.; Seyfried, C.E.; Morris, D.R.
J. Biol. Chem. 258, 12153-12162, 1983
A>Title: Regulation of protein synthesis in mitogen-activated bovine lymphocytes. Analysis
A:Reference number: A39105; MUID:84032385; PMID:6195151
A:Accession: A39105
A:Molecule type: mRNA
A:Residues: 76-227;344-374 <DEG>
A:Cross-references: GB:K00622; GB:K00623
C:Note: actins beta and gamma were not distinguished in this study
C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
C:Superfamily: actin
C:Keywords: blocked amino end; cell motility; cytoskeleton; methylated amino acid; micro
F:71/Modified site: blocked amino end (Asp) (probably acetylated) #status experimental
F:72/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 75; DB 1; Length 374;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFQOMWISKQ 15

Db 345 LASLSTFQOMWISKQ 359

RESULT 11

ATBOG
actin gamma - bovine (tentative sequence)
C:Species: Bos primigenius taurus (cattle)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: B14185; A02999
R:Vandekerckhove, J.; Weber, K.
Eur. J. Biochem. 90, 451-462, 1978
A>Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain
A:Reference number: A14185; MUID:79045349; PMID:213279
A:Accession: B14185
A:Molecule type: protein
A:Residues: 1-374 <VAN>
A:Cross-references: UNIPROT:P02571
A:Note: only peptides that differed in composition from the corresponding peptides of r
C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
C:Superfamily: actin
C:Keywords: blocked amino end; cell motility; cytoskeleton; methylated amino acid; micro
F:71/Modified site: blocked amino end (Glu) (probably acetylated) #status experimental
F:72/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 75; DB 1; Length 374;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFQOMWISKQ 15

Db 345 LASLSTFQOMWISKQ 359

RESULT 12

JC5818
gamma-actin - human
C:Species: Homo sapiens (man)
C>Date: 20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C:Accession: JC5818; PC4501
R:Hauschildt, S.; Schwarz, C.; Heine, H.; Ulmer, A.J.; Flad, H.D.; Rietschel, E.T.; Jen
Biochem. Biophys. Res. Commun. 241, 670-674, 1997
A>Title: Actin: A target of lipopolysaccharide-induced phosphorylation in human monocyte
A:Reference number: JC5818; MUID:98096379; PMID:9434766
A:Accession: JC5818
A:Molecule type: protein
A:Residues: 1-374 <HAU>
A:Cross-references: UNIPROT:P02571
A:Experimental source: monocyte
A:Accession: PC4501
A:Molecule type: protein
A:Residues: 1-61;84-112;147-190;196-209;215-253;335-358 <HA2>
A:Experimental source: monocyte

C;Comment: This protein is involved in a signal transduction that eventually leads to md
C;Superfamily: actin

Query Match 100.0%; Score 75; DB 2; Length 374;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASLSTFQQMWSKQ 15
|||||

Db 345 LASLSTFQQMWSKQ 359

RESULT 13

ATBOSM

actin, aortic smooth muscle - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 06-Sep-1996
C;Accession: A02997; S13480
R;Vandekerckhove, J.; Weber, K.
A;Title: The complete amino acid sequence of actins from bovine aorta, bovine heart, bovine skeletal muscle, and bovine brain.

A;Reference number: A02997; MUID:80047657; PMID:499690

A;Accession: A02997

A;Molecule type: protein

A;Residues: 1-375 <VAN>

R;Zevgoulis, V.G.; Sotiropoulis, T.G.; Evangelopoulos, A.E.

Biochim. Biophys. Acta 1091, 222-230, 1991

A;Title: Phosphorylase kinase from bovine stomach smooth muscle: a Ca (2+) -dependent protein

A;Reference number: S13480; MUID:91137633; PMID:1995080

A;Accession: S13480

A;Molecule type: protein

A;Residues: 40-49 <ZEV>

A;Experimental source: stomach

A;Note: this material appears to be actin of aortic smooth muscle type or a related molecule

C;Superfamily: actin

C;Keywords: acetylated amino end; methylated amino acid; muscle contraction

F;1/Modified site: acetylated amino end (Glu) #status predicted

F;73/Modified site: 3'-methylhistidine (His) #status experimental

Query Match 100.0%; Score 75; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASLSTFQQMWSKQ 15
|||||

Db 346 LASLSTFQQMWSKQ 360

RESULT 14

ATRTC

actin beta - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 22-Jun-1999
C;Accession: A38571; A02999
R;Nudel, U.; Zakut, R.; Shani, M.; Neuman, S.; Levy, Z.; Yaffe, D.
Nucleic Acids Res. 11, 1759-1771, 1983
A;Title: The nucleotide sequence of the rat cytoplasmic beta-actin gene.

A;Reference number: A38571; MUID:83168920; PMID:6300777

A;Accession: A38571

A;Molecule type: DNA

A;Residues: 1-375 <NUD>

A;Cross-references: GB:J00691; NID:G202653; PIDN:AAA40657.1; PID:G202654

C;Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,

C;Genetics:

A;Introns: 41/3; 121/3; 268/1; 328/3

C;Superfamily: actin

C;Keywords: cell motility; cytoskeleton; methylated amino acid; microfilament; mitosis;

F;2-375/Product: actin beta #status predicted <NAI>

F;73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 75; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASLSTFQQMWSKQ 15
|||||

Db 346 LASLSTFQQMWSKQ 360

RESULT 15

A48324

actin beta, cytoskeletal - common carp

C;Species: Cyprinus carpio (common carp)

C;Date: 03-Feb-1994 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004

C;Accession: A48324

R;Liou, Z.; Zhu, Z.; Roberg, K.; Faras, A.; Guise, K.; Kapuscinski, A.R.; Hackett, P.B.

DNA Seq. 1, 125-136, 1990

A;Title: Isolation and characterization of beta-actin gene of carp (Cyprinus carpio).

A;Reference number: A48324; MUID:92190540; PMID:2134183

A;Accession: A48324

A;Molecule type: DNA

A;Residues: 1-375 <LIU>

A;Cross-references: UNIPROT:P83750; GB:M24113; NID:G213041; PIDN:AAA68886.1; PID:G213042

A;Note: the authors translated the codon TTC for residue 21 as Pro, AAG for residue 50 as

7 as Pro

A;Note: the authors failed to translate the codon GGT for residue 42 as Gly

C;Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,

C;Genetics: 41/3; 121/3; 268/3; 328/3

A;Introns: 41/3; 121/3; 268/3; 328/3

C;Superfamily: actin

C;Keywords: acetylated amino end; cell motility; cytoskeleton; methylated amino acid; mi

F;2-375/Product: actin beta, cytoskeletal #status predicted <MAT>

F;2/Modified site: acetylated amino end (Asp) (in mature form) #status predicted

F;73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 75; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASLSTFQQMWSKQ 15
|||||

Db 346 LASLSTFQQMWSKQ 360

Search completed: April 8, 2005, 10:53:06

Job time : 9.33333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 57.8667 Seconds
(without alignments)
132.739 Million cell updates/sec

Title: US-09-423-351c-8
Perfect score: 75
Sequence: 1 LASLSTFOQMWSKQ 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	100.0	33	1 ACT_DICVI	Q24733 dictyocaulu
2	75	100.0	38	2 Q6VPP6	Q6VPP6 ixodes rici
3	75	100.0	45	2 Q6J0R3	Q6J0R3 hydra atten
4	75	100.0	45	2 Q6J0R4	Q6J0R4 hydra atten
5	75	100.0	50	2 Q9DDZ2	Q9DDZ2 micropterus
6	75	100.0	55	2 Q8AY69	Q8AY69 oncorhynchus
7	75	100.0	56	2 Q57575	Q57575 cynops pyrri
8	75	100.0	93	2 Q7ZZZ0	Q7ZZZ0 anas platyr
9	75	100.0	96	2 Q90X51	Q90X51 fundulus he
10	75	100.0	100	2 Q9TYD9	Q9TYD9 styela clav
11	75	100.0	106	2 Q80UA7	Q80UA7 marmota mon
12	75	100.0	113	2 Q6Y260	Q6Y260 pagrus majo
13	75	100.0	123	2 Q6UIS1	Q6UIS1 macaca mula
14	75	100.0	123	2 Q8UIS2	Q8UIS2 pan troglod
15	75	100.0	124	2 Q9DFK3	Q9DFK3 gillichthys
16	75	100.0	131	2 Q9XSB1	Q9XSB1 tupia glis
17	75	100.0	134	2 Q99NC5	Q99NC5 mus musculu
18	75	100.0	134	2 Q99NC6	Q99NC6 rattus norv
19	75	100.0	149	2 Q6PTC1	Q6PTC1 sitobion av
20	75	100.0	149	2 Q6PTC2	Q6PTC2 sitobion av
21	75	100.0	154	1 ACT4_LYTPI	Q25380 lytechinus
22	75	100.0	159	2 Q96DE1	Q96DE1 homo sapien
23	75	100.0	165	2 Q96FU6	Q96FU6 homo sapien
24	75	100.0	172	1 ACT3_LYTPI	Q25379 lytechinus
25	75	100.0	172	1 ACTM_LYTPI	Q25381 lytechinus
26	75	100.0	181	2 Q6XJ33	Q6XJ33 drosophila
27	75	100.0	195	2 Q7M3B0	Q7M3B0 sus scrofa
28	75	100.0	213	2 Q7M3Y7	Q7M3Y7 styela clav
29	75	100.0	243	2 Q8MVP7	Q8MVP7 boltenia vi
30	75	100.0	244	2 Q94FN6	Q94FN6 lotharella
31	75	100.0	257	2 Q9P443	Q9P443 aspergillus

Q6JXI0 hedriocysti
Q6JXI1 clathrulina
Q6JXI2 raphidiophr
Q6J143 homo sapien
Q6WY5 ophiostoma
Q96WY6 ophiostoma
Q96WY6 ophiostoma
Q85W8 lama glama
Q85W8 lama glama
Q18513 heliocidari
Q8WRE6 culicoides
Q4546 mustela put
Q6YMS6 littorina 1
P18602 artemia sp.
Q6BSW7 debaryomyce

ALIGNMENTS

RESULT 1

ACT_DICVI
ID ACT_DICVI STANDARD; PRT; 33 AA.
AC Q24733;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Actin (Fragment).
OS Dictyocaulus viviparus (Bovine lungworm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC Trichostrongyloidea; Dictyocaulidae; Dictyocaulinae; Dictyocaulus.
OX NCBI_TaxID=29172;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Larva;
RA von Samson-Hammelstjerna G., Wunderlich G., Muehlethleget F.,
RA Froesch M., Schnieder T.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the actin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U40590; AAA83551.1; -
CC InterPro; IPR004001; Actin.
CC InterPro; IPR004000; Actin_like.
CC Pfam; PF00022; Actin; 1.
CC PROSITE; PS00406; ACTINS_1; PARTIAL.
CC PROSITE; PS00432; ACTINS_2; 1.
CC PROSITE; PS01132; ACTINS_ACT_LIKE; PARTIAL.
CC Structural protein.
CC NON TER 1
SQ SEQUENCE 33 AA; 3830 MW; 72E2DB4D5D5CDAEC CRC64;

Query Match 100.0%; Score 75; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 8.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASLSTFOQMWSKQ 15

DB 4 LASLSTFOQMWSKQ 18

RESULT 2

Q6VPP6

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ID Q6VPP6 PRELIMINARY; PRT; 38 AA.
AC Q6VPP6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Gamma actin-like protein (Fragment).
OS Ixodes ricinus (Sheep tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Ixodes.
OX NCBI_TaxID=34613;
RN [1]
RP SEQUENCE FROM N.A.
RA Rudenko N.K., Golovchenko M.P., Edwards M.J., Grubhoffer L.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY333957; AAQ23081.1; -.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR PROSITE; PS00432; ACTINS_2; 1.
FT NON_TER 1
SQ SEQUENCE 38 AA; 4331 MW; D52BA0C57DC38864 CRC64;

Query Match 100.0%; Score 75; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 9.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFQQMWSKQ 15
Db 9 LASLSTFQQMWSKQ 23
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RESULT 3
Q6JOR3 PRELIMINARY; PRT; 45 AA.
AC Q6JOR3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Actin 1.7 (Fragment).
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC Hydridae; Hydra.
OX NCBI_TaxID=6087;
RN [1]
RP SEQUENCE FROM N.A.
RA Fisher D.A., Bode H.R.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY609159; AAT37544.1; -.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR PROSITE; PS00432; ACTINS_2; 1.
FT NON_TER 1
SQ SEQUENCE 45 AA; 5159 MW; 7796DEF78D574D0 CRC64;

Query Match 100.0%; Score 75; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFQQMWSKQ 15
Db 16 LASLSTFQQMWSKQ 30
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RESULT 4
Q6JOR4 PRELIMINARY; PRT; 45 AA.
AC Q6JOR4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Actin 1.6 (Fragment).
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC Hydridae; Hydra.
OX NCBI_TaxID=6087;
RN [1]
RP SEQUENCE FROM N.A.
RA Fisher D.A., Bode H.R.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY609159; AAT37544.1; -.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR PROSITE; PS00432; ACTINS_2; 1.
FT NON_TER 1
SQ SEQUENCE 45 AA; 5159 MW; 7796DEF78D574D0 CRC64;

Query Match 100.0%; Score 75; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFQQMWSKQ 15
Db 16 LASLSTFQQMWSKQ 30
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RESULT 5
Q9DDZ2 PRELIMINARY; PRT; 50 AA.
AC Q9DDZ2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta-actin (Fragment).
OS Micropterus salmoides (Largemouth bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Centrarchidae; Micropterus.
OX NCBI_TaxID=27706;
RN [1]
RP SEQUENCE FROM N.A.
RA Bowman C.J., Sabo-Attwood T.L., Lee H.S., Denalow N.D.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF253319; AAG44624.1; -.
DR HSSP; P02568; IMA9.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 1
FT NON_TER 50
SQ SEQUENCE 50 AA; 5694 MW; 44542890573899BB CRC64;

Query Match 100.0%; Score 75; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFQQMWSKQ 15
Db 16 LASLSTFQQMWSKQ 30
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Query Match 100.0%; Score 75; DB 2; Length 50;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFQOMWISKQ 15
 Db 35 LASLSTFQOMWISKQ 49

RESULT 6

QAY69 PRELIMINARY; PRT; 55 AA.

AC Q8AY69;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Beta-actin (Fragment).
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Schwindt A.R., Alonso M., Leong J.C., Schreck C.B.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF550583; AAN74801.1; -;
 DR HSSP; P02568; IMA9.
 DR GO; GO:0015629; C:actin cytoskeleton; IEA.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
 DR InterPro; IPR004000; Actin_like.
 DR Pfam; PF00022; Actin.1.
 FT NON TER 1
 FT NON TER 55
 SQ SEQUENCE 55 AA; 6163 MW; 9A4319FB34DD79D8 CRC64;

Query Match 100.0%; Score 75; DB 2; Length 55;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFQOMWISKQ 15
 Db 40 LASLSTFQOMWISKQ 54

RESULT 7

O57575 PRELIMINARY; PRT; 56 AA.

AC O57575;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Alpha cardiac actin (Fragment).
 OS Cynops pyrrhogaster (Japanese common newt).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
 OX NCBI_TaxID=8330;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mizuno M., Takabatake T., Takahashi T.C., Takeshima K.;
 RT "pax-6 gene expression in newt eye development.";
 RL Dev. Genes Evol. 207:167-176(1997).
 DR EMBL; D64017; BAA24031.1; -;
 DR HSSP; P02568; ILCU.
 DR GO; GO:0005884; C:actin filament; IEA.
 DR GO; GO:0003774; F:motor activity; IEA.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
 DR InterPro; IPR004001; Actin.
 DR InterPro; IPR004000; Actin_like.
 DR Pfam; PF00022; Actin.1.
 DR PROSITE; PS00432; ACTINS_2; 1.

FT NON TER 1
 SQ SEQUENCE 56 AA; 6339 MW; 3532A4205AC50E5 CRC64;

Query Match 100.0%; Score 75; DB 2; Length 56;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFQOMWISKQ 15
 Db 27 LASLSTFQOMWISKQ 41

RESULT 8

Q7ZZZ0 PRELIMINARY; PRT; 93 AA.

AC Q7ZZZ0;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Beta-actin (Fragment).
 OS Anas platyrhynchos (Domestic duck).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
 OX NCBI_TaxID=8839;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Sreekumar E., Premraj A., Rasool T.J.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY251275; AAP04479.1; -;
 DR HSSP; P02568; 1QZ5.
 DR GO; GO:0005884; C:actin filament; IEA.
 DR GO; GO:0003774; F:motor activity; IEA.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
 DR InterPro; IPR004001; Actin.
 DR InterPro; IPR004000; Actin_like.
 DR Pfam; PF00022; Actin.1.
 DR PROSITE; PS00432; ACTINS_2; 1.
 FT NON TER 1
 FT NON TER 93
 SQ SEQUENCE 93 AA; 10444 MW; F867ADF144D80523 CRC64;

Query Match 100.0%; Score 75; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 2.4e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFQOMWISKQ 15
 Db 64 LASLSTFQOMWISKQ 78

RESULT 9

Q90X51 PRELIMINARY; PRT; 96 AA.

AC Q90X51;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Beta-actin (Fragment).
 OS Fundulus heteroclitus (Killifish) (Mummichog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
 OC Cyprinodontiformes; Fundulidae; Fundulus.
 OX NCBI_TaxID=8078;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Rolling J.A., Baldwin W.S.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF435092; AAL29465.1; -;
 DR HSSP; P02568; 1QZ5.
 DR GO; GO:0005884; C:actin filament; IEA.
 DR GO; GO:0003774; F:motor activity; IEA.

DR GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR Pfam: PF00022; Actin; 1.
DR PROSITE: PS00432; ACTINS_2; 1.
FT NON_TER 1
SQ SEQUENCE 96 AA; 10798 MW; 7440DA6AE5A070C4 CRC64;

Query Match 100.0%; Score 75; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 2.5e-05; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LASLSTFQQMWSKQ 15
Db 78 LASLSTFQQMWSKQ 92

RESULT 10
Q9TYD9 PRELIMINARY; PRT; 100 AA.
AC Q9TYD9; 100 AA.
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Alpha-muscle actin (Fragment).
GN Name=TB24;
OS Styela clava (sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Styelidae; Styela.
OX NCBI_TaxID=7725;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92249656; PubMed=1577198;
RA Beach R.L., Jeffery W.R.;
RT "Multiple actin genes encoding the same alpha-muscle isoform are expressed during ascidian development.";
RL Dev. Biol. 151:55-66 (1992).
DR EMBL: L13788; AAA29846.1; -.
DR HSP: P02568; IQ25.
DR GO:0005884; C:actin filament; IEA.
DR GO:0003774; F:motor activity; IEA.
DR GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro: IPR004001; Actin.
DR Pfam: PF00022; Actin; 1.
DR PROSITE: PS00432; ACTINS_2; 1.
FT NON_TER 1
SQ SEQUENCE 100 AA; 11264 MW; 108CE34548BABB5E CRC64;

Query Match 100.0%; Score 75; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 2.6e-05; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LASLSTFQQMWSKQ 15
Db 71 LASLSTFQQMWSKQ 85

RESULT 11
Q80UA7 PRELIMINARY; PRT; 106 AA.
AC Q80UA7;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Beta-actin (Fragment).
OS Marmota monax (woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22554704; PubMed=12668969; DOI=10.1053/jhep.2003.50154;

RA Wang Y., Menne S., Jacob J.R., Tennant B.C., Gerin J.L., Cote P.J.;
RT "Role of type 1 versus type 2 immune responses in liver during the onset of chronic woodchuck hepatitis virus infection.";
RL Hepatology 37:771-780 (2003).
DR EMBL: AY170121; AAC039434.1; -.
DR HSP: P10983; 1D4X.
DR GO:0005884; C:actin filament; IEA.
DR GO:0003774; F:motor activity; IEA.
DR GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro: IPR004001; Actin.
DR Pfam: PF00022; Actin; 1.
DR PROSITE: PS00432; ACTINS_2; 1.
FT NON_TER 1
SQ SEQUENCE 106 AA; 11864 MW; 9FFDC145651FE343 CRC64;

Query Match 100.0%; Score 75; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.8e-05; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFQQMWSKQ 15
Db 77 LASLSTFQQMWSKQ 91

RESULT 12
Q6Y260 PRELIMINARY; PRT; 113 AA.
AC Q6Y260;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Alpha-actin protein (Fragment).
OS Pagrus major (Red sea bream) (Chrysophrys major).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Pagrus.
OX NCBI_TaxID=143350;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Chen S.L., Xu M.Y., Hu S.L., Li L.;
RT "Analysis of immune-relevant genes expressed in red sea bream spleen.";
RL Aquaculture 240:115-130 (2004).
DR EMBL: AY190676; AAF20152.1; -.
DR GO:0005884; C:actin filament; IEA.
DR GO:0003774; F:motor activity; IEA.
DR GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro: IPR004001; Actin.
DR PROSITE: PS00432; ACTINS_2; 1.
FT NON_TER 1
SQ SEQUENCE 113 AA; 12550 MW; 4C796A5B5B35269F CRC64;

Query Match 100.0%; Score 75; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.9e-05; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFQQMWSKQ 15
Db 84 LASLSTFQQMWSKQ 98

RESULT 13
Q6UIS1 PRELIMINARY; PRT; 123 AA.
AC Q6UIS1;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Actin beta subunit (Fragment).
GN Name=ACTB;

OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22946167; PubMed=14557539; DOI=10.1073/pnas.2135499100;
 RA Caceres M., Lachuer J., Zapala M.A., Redmond J.C., Kudo L.,
 RA Geschwind D.H., Lockhart D.J., Preuss T.M., Barlow C.;
 RT "Elevated gene expression levels distinguish human from non-human
 primate brains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:13030-13035(2003).
 DR EMBL; AY369786; AAR1122.1; -;
 DR GO; GO:0005884; C:actin filament; IEA.
 DR GO; GO:0003774; F:motor activity; IEA.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
 DR InterPro; IPR004001; Actin.
 DR InterPro; IPR004000; Actin_like.
 DR SMART; SM00268; ACTIN; 1.
 DR PROSITE; PS00432; ACTINS_2; 1.
 FT NON TER 1
 SQ SEQUENCE 123 AA; 13874 MW; BBOA1DA9C05599E1 CRC64;

Query Match 100.0%; Score 75; DB 2; Length 123;
 Best Local Similarity 100.0%; Pred. No. 3.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFOQMWSKQ 15
 Db 94 LASLSTFOQMWSKQ 108
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 |||||

RESULT 14
 Q6UIS2 PRELIMINARY; PRT; 123 AA.
 AC Q6UIS2;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Actin beta subunit (Fragment).
 GN Name=ACTB;
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22946167; PubMed=14557539; DOI=10.1073/pnas.2135499100;
 RA Caceres M., Lachuer J., Zapala M.A., Redmond J.C., Kudo L.,
 RA Geschwind D.H., Lockhart D.J., Preuss T.M., Barlow C.;
 RT "Elevated gene expression levels distinguish human from non-human
 primate brains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:13030-13035(2003).
 DR EMBL; AY369785; AAR1122.1; -;
 DR GO; GO:0005884; C:actin filament; IEA.
 DR GO; GO:0003774; F:motor activity; IEA.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
 DR InterPro; IPR004001; Actin.
 DR InterPro; IPR004000; Actin_like.
 DR SMART; SM00268; ACTIN; 1.
 DR PROSITE; PS00432; ACTINS_2; 1.
 FT NON TER 1
 SQ SEQUENCE 123 AA; 13874 MW; BBOA1DA9C05599E1 CRC64;

Query Match 100.0%; Score 75; DB 2; Length 123;
 Best Local Similarity 100.0%; Pred. No. 3.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFOQMWSKQ 15
 Db 94 LASLSTFOQMWSKQ 108
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 |||||

RESULT 15
 Q9DFK3 PRELIMINARY; PRT; 124 AA.
 AC Q9DFK3;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DE Skeletal alpha-actin (Fragment).
 OS Gillichthys mirabilis (Long-jawed mudsucker).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Gobioidel;
 OC Gobiidae; Gillichthys.
 OX NCBI_TaxID=8222;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal white muscle;
 RX MEDLINE=21117151; PubMed=11172064; DOI=10.1073/pnas.98.4.1993;
 RA Gracey A.Y., Troll J.V., Somero G.N.;
 RT "Hypoxia-induced gene expression profiling in the euryoxic fish
 Gillichthys mirabilis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:1993-1998(2001).
 DR EMBL; AF286232; AAG13352.1; -;
 DR HSSP; P02568; 1025.
 DR GO; GO:0015629; C:actin cytoskeleton; IEA.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
 DR InterPro; IPR004000; Actin_like.
 DR Pfam; PF00022; Actin; 1.
 FT NON TER 1
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Query Match 100.0%; Score 75; DB 2; Length 124;
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Qy 1 LASLSTFOQMWSKQ 15
 Db 95 LASLSTFOQMWSKQ 109
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Search completed: April 8, 2005, 12:03:11
 Job time : 58.8667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 62.4 Seconds
(without alignments)
92.971 Million cell updates/sec

Title: US-09-423-351C-9

Perfect score: 76

Sequence: 1 DEAQSRGILTLKYP 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	100.0	15	2 AAW92535	Beta-acti
2	76	100.0	54	3 AAG18905	Aag18905 Zea mays
3	76	100.0	58	3 AAG18945	Aag18945 Zea mays
4	76	100.0	73	3 AAG27057	Aag27057 Zea mays
5	76	100.0	74	3 AAG18936	Aag18936 Zea mays
6	76	100.0	75	3 AAG18944	Aag18944 Zea mays
7	76	100.0	79	3 AAG12594	Aag12594 Zea mays
8	76	100.0	82	3 AAG18904	Aag18904 Zea mays
9	76	100.0	88	3 AAG18916	Aag18916 Zea mays
10	76	100.0	91	3 AAG18935	Aag18935 Zea mays
11	76	100.0	95	3 AAG19142	Aag19142 Zea mays
12	76	100.0	96	3 AAG12593	Aag12593 Zea mays
13	76	100.0	99	3 AAG18903	Aag18903 Zea mays
14	76	100.0	101	3 AAG27056	Aag27056 Zea mays
15	76	100.0	105	5 ABP42469	Abp42469 Human ova
16	76	100.0	108	4 AAM18324	Aam18324 Peptide #
17	76	100.0	108	4 ABB37358	Abb37358 Peptide #
18	76	100.0	108	4 AAM30812	Aam30812 Peptide #
19	76	100.0	108	4 ABB32106	Abb32106 Peptide #
20	76	100.0	108	4 ABB22644	Abb22644 Protein #
21	76	100.0	108	4 AAM70488	Aam70488 Human bon
22	76	100.0	108	4 AAM58048	Aam58048 Human bra
23	76	100.0	108	4 ABG52170	Abg52170 Human liv
24	76	100.0	108	4 AAM05932	Aam05932 Peptide #
25	76	100.0	108	5 ABG40127	Abg40127 Human pep

26	76	100.0	111	3 AAG19141	Aag19141 Zea mays
27	76	100.0	116	3 AAG18915	Aag18915 Zea mays
28	76	100.0	118	3 AAG27055	Aag27055 Zea mays
29	76	100.0	133	3 AAG18914	Aag18914 Zea mays
30	76	100.0	150	4 AAG15101	Abg15101 Novel hum
31	76	100.0	157	4 ABB66853	Abb66853 Drosophil
32	76	100.0	166	4 AAG26869	Abg26869 Novel hum
33	76	100.0	167	4 AAU33077	Aau33077 Novel hum
34	76	100.0	201	5 ABP43176	Abp43176 Human ova
35	76	100.0	204	5 ABP43016	Abp43016 Human ova
36	76	100.0	211	7 ABM73899	Abm73899 DNA clone
37	76	100.0	219	8 ABO58422	Abos58422 Human gen
38	76	100.0	239	7 ADE31206	Ades31206 Human dia
39	76	100.0	258	4 AEG00383	Aeg00383 Novel hum
40	76	100.0	276	3 AAG50947	Aag50947 Arabidops
41	76	100.0	277	3 AAG05115	Aag05115 Arabidops
42	76	100.0	304	3 AAG50946	Aag50946 Arabidops
43	76	100.0	305	3 AAG05114	Aag05114 Arabidops
44	76	100.0	308	3 AAG37210	Aag37210 Arabidops
45	76	100.0	311	3 AAG37209	Aag37209 Arabidops

ALIGNMENTS

RESULT 1

AAW92535

ID AAW92535 standard; peptide; 15 AA.

XX AC AAW92535;

DT 26-APR-1999 (first entry)

DE Beta-actin reference peptide substrate #9.

XX Peptide substrate; CCT; eukaryotic type II chaperonin complex; cyclin;

KW binding agent; substrate-binding site; SBS; substrate folding; actin;

KW tubulin; treatment; cancer; anticancer drug; viral infection; screening;

KW reduced toxicity.

OS Synthetic.

XX WO9853322-A1.

PN 26-NOV-1998.

XX 22-MAY-1998; 98WO-GB001485.

XX 23-MAY-1997; 97GB-00010762.

XX (CANC-) INST CANCER RES ROYAL CANCER HOSPITAL.

XX Willison K, Hynes G, Liou AK;

XX WPI; 1999-070162/06.

Identifying specific binding agents for substrate binding site in CCT chaperonin complex - also new peptide binding agents and their mimetics, and peptides containing a specific CCT binding site, used for treating cancer.

XX Disclosure; Fig 10; 97pp; English.

This invention describes a method which uses the CCT (eukaryotic type II chaperonin) complex or part of it, for identifying a binding agent that can occupy a substrate-binding site (SBS) on the CCT complex. By binding to the CCT complex, the binding agents block an SBS so that biological activity of the CCT complex is affected, particularly its ability to fold substrates such as actin, tubulin and cyclin. The binding agents are useful for treatment of cancer, particularly when used in combination with an anticancer drug, or viral infections. Nucleic acid fragments are used to screen for agents, e.g. binding agents that modulate interaction between the CCT complex and a protein that is to be folded. The binding

CC agents may target cells that are actively synthesising tubulin etc.
 CC (unlike known microtubule-stabilising agents that affect all cells), so
 CC should have reduced toxicity for normal cells. AAW92527-W92541 are
 CC peptide substrates used in the method of the invention

XX Sequence 15 AA;

Query Match 100.0%; Score 76; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 7.9e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEAQSKRGILTLKYP 15
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 Db 1 DEAQSKRGILTLKYP 15

RESULT 2
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 ID AAG18905 standard; protein; 54 AA.

XX AC AAG18905;

XX DT 17-OCT-2000 (first entry)

XX DE Zea mays protein fragment SEQ ID NO: 20499.

XX KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence; corn.

XX OS Zea mays subsp. mays.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.

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Query Match 100.0%; Score 76; DB 3; Length 54;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 13 DEAQSKRGILTLYP 27

RESULT 3
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ID AAG18945 standard; protein; 58 AA.
XX
AC AAG18945;
XX
DT 17-OCT-2000 (first entry)
XX
DE Zea mays protein fragment SEQ ID NO: 20555.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
PN EP1033405-A2.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-00301439.
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
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hybridisation assay; genetic mapping; gene expression control; promoter;
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KW termination sequence; corn.
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Query Match 100.0%; Score 76; DB 3; Length 79;

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Query Match 100.08; Score 76; DB 3; Length 82;

Best Local Similarity 100.08; Pred. No. 5e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEAQSKRGILTKYP 15

Db 41 DEAQSKRGILTKYP 55

RESULT 9

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 ID AAG18916 standard; protein; 88 AA.

XX AC AAG18916;

XX AC AAG18916;

DT 17-OCT-2000 (first entry)

DE Zea mays protein fragment SEQ ID NO: 20514.

XX Zea mays protein fragment SEQ ID NO: 20514.

KW Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence; corn.

OS Zea mays subsp. mays.

XX Zea mays subsp. mays.

PN EP1033405-A2.

XX EP1033405-A2.

PD 06-SEP-2000.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0121825P.

PR 21-APR-1999; 99US-0130449P.
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Query Match 100.0%; Score 76; DB 3; Length 88;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEAQSKRGILTLYP 15
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RESULT 10

AAG18935
ID AAG18935 standard; protein; 91 AA.

XX AC AAG18935;

XX DT 17-OCT-2000 (first entry)

XX DE Zea mays protein fragment SEQ ID NO: 20541.

XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence; corn.

XX OS Zea mays subsp. mays.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX XX 25-FEB-1999; 99US-0121825P.

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PR 06-APR-1999; 99US-0128234P.

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Fri Apr 8 14:14:34 2005

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PR	19-MAY-1999;	99US-0134941P.	PR	02-AUG-1999;	99US-0146386P.
PR	20-MAY-1999;	99US-0135124P.	PR	02-AUG-1999;	99US-0146388P.
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PR	28-MAY-1999;	99US-0136782P.	PR	05-AUG-1999;	99US-0147302P.
PR	01-JUN-1999;	99US-0137222P.	PR	05-AUG-1999;	99US-0147260P.
PR	03-JUN-1999;	99US-0137528P.	PR	06-AUG-1999;	99US-0147303P.
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XX DT 17-OCT-2000 (first entry)

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 KW termination sequence; corn.

XX OS Zea mays subsp. mays.

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18-JUN-1999; 99US-0139461P.
18-JUN-1999; 99US-0139462P.
18-JUN-1999; 99US-0139463P.
18-JUN-1999; 99US-0139750P.
18-JUN-1999; 99US-0139763P.
21-JUN-1999; 99US-0139817P.
22-JUN-1999; 99US-0139859P.
23-JUN-1999; 99US-0140353P.
23-JUN-1999; 99US-0140354P.
24-JUN-1999; 99US-0140695P.
28-JUN-1999; 99US-0140823P.
29-JUN-1999; 99US-0140991P.
30-JUN-1999; 99US-0141287P.
01-JUL-1999; 99US-0141842P.
01-JUL-1999; 99US-0142154P.
02-JUL-1999; 99US-0142055P.
06-JUL-1999; 99US-0142390P.
08-JUL-1999; 99US-0142803P.
09-JUL-1999; 99US-0142920P.
12-JUL-1999; 99US-0142977P.
13-JUL-1999; 99US-0143542P.
14-JUL-1999; 99US-0143624P.
15-JUL-1999; 99US-0144005P.
16-JUL-1999; 99US-0144085P.
16-JUL-1999; 99US-0144086P.
19-JUL-1999; 99US-0144325P.
19-JUL-1999; 99US-0144331P.
19-JUL-1999; 99US-0144332P.
19-JUL-1999; 99US-0144333P.
19-JUL-1999; 99US-0144334P.
19-JUL-1999; 99US-0144335P.
20-JUL-1999; 99US-0144352P.
20-JUL-1999; 99US-0144632P.
20-JUL-1999; 99US-0144884P.
21-JUL-1999; 99US-0144814P.
21-JUL-1999; 99US-0145086P.
21-JUL-1999; 99US-0145088P.
22-JUL-1999; 99US-0145085P.
22-JUL-1999; 99US-0145087P.
22-JUL-1999; 99US-0145089P.
22-JUL-1999; 99US-0145192P.
23-JUL-1999; 99US-0145145P.
23-JUL-1999; 99US-0145218P.
23-JUL-1999; 99US-0145224P.
26-JUL-1999; 99US-0145276P.
27-JUL-1999; 99US-0145913P.
27-JUL-1999; 99US-0145918P.
27-JUL-1999; 99US-0145919P.
28-JUL-1999; 99US-0145951P.
02-AUG-1999; 99US-0146386P.
02-AUG-1999; 99US-0146388P.
02-AUG-1999; 99US-0146389P.
03-AUG-1999; 99US-0147038P.
04-AUG-1999; 99US-0147204P.
04-AUG-1999; 99US-0147302P.
05-AUG-1999; 99US-0147152P.
05-AUG-1999; 99US-0147260P.
06-AUG-1999; 99US-0147303P.
06-AUG-1999; 99US-0147416P.
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PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155689P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156598P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 21-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160811P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 100.0%; Score 76; DB 3; Length 99;
Beat Local Similarity 100.0%; Pred. No. 6.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QV 1 DEAQSKRGILTLYP 15
Db 58 DEAQSKRGILTLYP 72
RESULT 14
AAG27056
ID AAG27056 standard; protein; 101 AA.
XX
AC AAG27056;
XX
DT 17-OCT-2000 (first entry)
XX
DE Zea mays protein fragment SEQ ID NO: 31746.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.

ID ABP42469 standard; protein; 105 AA.
 AC ABP42469;
 XX
 DT 22-AUG-2002 (first entry)
 XX
 DE Human ovarian antigen HOCQ94, SEQ ID NO:3601.
 XX
 KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis; neuroprotective;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive.
 XX
 OS Homo sapiens.
 XX
 PN WO200200677-A1.
 XX
 PD 03-JAN-2002.
 XX
 PF 07-JUN-2001; 2001WO-US018569.
 XX
 PR 07-JUN-2000; 2000US-0209467P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Birse CE, Rosen CA;
 XX
 DR WPI; 2002-147878/19.
 DR N-PSDB; ABQ55546.
 XX
 PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 PT cancer), immune disorders, cardiovascular disorders and neurological
 PT diseases.
 XX
 PS Claim 11; SEQ ID NO 3601; 2922pp; English.
 XX
 CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovary and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 105 AA;
 Query Match 100.0%; Score 76; DB 5; Length 105;
 Best Local Similarity 100.0%; Pred. No. 6.5e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DEAQSKRGILTLKYP 15
 Db 57 DEAQSKRGILTLKYP 71
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 Job time : 63.4 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 62.4 Seconds
(without alignments)
92.971 Million cell updates/sec

Title: US-09-423-351C-8

Perfect score: 75

Sequence: 1 LASLSTFQQMWISKQ 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	75	100.0	15	2 AAW92534	Aaw92534 Beta-acti
2	75	100.0	48	8 ADP81223	Adp81223 Protein o
3	75	100.0	86	4 ABG08617	Abg08617 Novel hum
4	75	100.0	110	5 ABP42928	Abp42928 Human ova
5	75	100.0	129	4 AAM81819	Aam81819 Human hae
6	75	100.0	135	4 AAU32061	Aau32061 Novel hum
7	75	100.0	145	5 ABP43127	Abp43127 Human ova
8	75	100.0	147	4 AAM80875	Aam80875 Human hae
9	75	100.0	147	4 AAM81886	Aam81886 Human hae
10	75	100.0	147	4 AAM81332	Aam81332 Human hae
11	75	100.0	149	8 ABO84771	Abo84771 Human can
12	75	100.0	181	4 ABG11441	Abg11441 Novel hum
13	75	100.0	197	6 ADA55146	Ada55146 Human pro
14	75	100.0	250	4 ABG08618	Abg08618 Novel hum
15	75	100.0	274	6 ABU70549	Abu70549 Human adi
16	75	100.0	278	4 ABG15466	Abg15466 Novel hum
17	75	100.0	279	4 ABG11440	Abg11440 Novel hum
18	75	100.0	294	7 ADI63068	Adi63068 Human apo
19	75	100.0	332	6 ADI63011	Adi63011 Human apo
20	75	100.0	334	6 ABP98860	Abp98860 Human str
21	75	100.0	374	3 AAB12985	Aab12985 Human bet
22	75	100.0	375	1 AAP61532	Aap61532 Sequence
23	75	100.0	375	2 AAR22026	Aar22026 A. chryso
24	75	100.0	375	2 AAR22096	Aar22096 Actin. 3/
25	75	100.0	375	2 AAR49248	Aar49248 Actin. 3/

ALIGNMENTS

RESULT 1

AAW92534
ID AAW92534 standard; peptide; 15 AA.

AC AAW92534;

XX
XX 26-APR-1999 (first entry)

DE Beta-actin reference peptide substrate #8.

XX Peptide substrate; CCT; eukaryotic type II chaperonin complex; cyclin;
KW binding agent; substrate-binding site; SBS; substrate folding; actin;
KW tubulin; treatment; cancer; anticancer drug; viral infection; screening;
KW reduced toxicity.

XX Synthetic.

XX WO9853322-A1.

XX 26-NOV-1998.

XX 22-MAY-1998; 98WO-GB001485.

XX 23-MAY-1997; 97GB-00010762.

XX (CANC-) INST CANCER RES ROYAL CANCER HOSPITAL.

XX Willison K, Hynes G, Liou AK;

XX WPI; 1999-070162/06.

PT Identifying specific binding agents for substrate binding site in CCT
PT chaperonin complex, also new peptide binding agents and their mimetics,
PT and peptides containing a specific CCT binding site, used for treating
cancer.

XX Disclosure; Fig 10; 97pp; English.

CC This invention describes a method which uses the CCT (eukaryotic type II
CC chaperonin) complex or part of it, for identifying a binding agent that
CC can occupy a substrate-binding site (SBS) on the CCT complex. By binding
CC to the CCT complex, the binding agents block an SBS so that biological
CC activity of the CCT complex is affected, particularly its ability to fold
CC substrates such as actin, tubulin and cyclin. The binding agents are
CC useful for treatment of cancer, particularly when used in combination
CC with an anticancer drug, or viral infections. Nucleic acid fragments are
CC used to screen for agents, e.g. binding agents that modulate interaction
CC between the CCT complex and a protein that is to be folded. The binding

Aar50328 Drug resi
Aaw77100 P. chryso
Aaw77101 A. chryso
Aaw59176 P. calini
Aab15017 Posttrans
Aay94569 Human car
Aab15016 Posttrans
Aab577395 Human act
Aab64271 Angiogene
Abm04830 Rat cytop
Adb85212 Rat actin
Ade61174 Rat Prote
Adf30525 Rat angio
Adi62970 Human apo
Adi62970 Human apo
Adi63040 Human apo
Adi13002 Human ste
Adi78489 Actin pro
Adl14103 Human ear
Adn04506 Antipsori

CC agents may target cells that are actively synthesising tubulin etc.
 CC (unlike known microtubule-stabilising agents that affect all cells), so
 CC should have reduced toxicity for normal cells. AAW92527-W92541 are
 CC peptide substrates used in the method of the invention
 XX
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 75; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6.5e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LASLSTFOQMWSKQ 15
 DB 1 LASLSTFOQMWSKQ 15
 RESULT 2
 ADP81223
 ID ADP81223 standard; protein; 48 AA.
 XX
 AC ADP81223;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Protein of human ovarian specific gene, SEQ ID No 257.
 XX normal; neoplastic; ovarian; ovarian specific nucleic acid; OSNA;
 KW metastatic; cancer; vaccine; cytostatic; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2004053079-A2.
 XX
 PD 24-JUN-2004.
 XX
 PF 08-DEC-2003; 2003WO-US038855.
 XX
 PR 06-DEC-2002; 2002US-0431301P.
 PR 06-DEC-2002; 2002US-0431321P.
 PR 30-JUN-2003; 2003US-0484584P.
 PR 07-NOV-2003; 2003US-0518607P.
 XX
 PA (DIAD-) DIADEXUS INC.
 XX
 PI Macina RA, Turner LR, Sun Y, Liu S, Chen H;
 XX
 DR WPI; 2004-468850/44.
 DR N-PSDB; ADP81063.
 XX
 PT New ovarian specific nucleic acid molecules and polypeptides useful for
 PT diagnosing, preventing or treating ovarian cancer, for producing
 PT transgenic animals or cells, or for research purposes.
 XX
 PS Claim 12; SEQ ID NO 257; 754pp; English.
 XX
 CC The invention relates to novel isolated nucleic acid molecules and
 CC polypeptides present in normal and neoplastic ovarian cells. These
 CC comprise a nucleic acid sequence encoding any of the 167 amino acid
 CC sequences (e.g. 438, 237 or 233 amino acids) fully defined in the
 CC specification (SEQ. ID NOS: ADP81095 to ADP81261) and comprises any of
 CC the 128 nucleotide sequences (e.g. 4798, 1494 or 1691 bp) fully defined
 CC in the specification (SEQ. ID NOS: ADP80967 to ADP81094). The invention
 CC further comprises a method for determining the presence of a ovarian
 CC specific nucleic acid (OSNA) in a sample; a vector comprising the above
 CC nucleic acid molecule; a host cell comprising the vector; a method for
 CC producing a polypeptide encoded by the above nucleic acid molecule; a
 CC polypeptide encoded by the nucleic acid molecule cited above; an antibody
 CC or its fragment that specifically binds to the above polypeptide; a
 CC method for determining the presence of an ovarian specific protein in a
 CC sample; a method for diagnosing or monitoring the presence and metastases
 CC of ovarian cancer in a patient; a kit for detecting a risk of cancer or
 CC presence of cancer in a patient, the kit comprising a means for
 CC determining the presence of the above nucleic acid molecule or

CC polypeptide; a method of treating a patient with ovarian cancer; and a
 CC vaccine comprising the above polypeptide or nucleic acid encoding the
 CC polypeptide. The isolated nucleic acid molecules and polypeptides have
 CC cytostatic activity. The isolated polypeptides may be used to create a
 CC vaccine. The isolated nucleic acid molecules and polypeptides can be used
 CC for diagnosing or monitoring the presence and metastases of ovarian
 CC cancer and treating ovarian cancer. This sequence represents the protein
 CC of an ovarian specific gene of the invention.
 XX
 SQ Sequence 48 AA;
 Query Match 100.0%; Score 75; DB 8; Length 48;
 Best Local Similarity 100.0%; Pred. No. 2.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LASLSTFOQMWSKQ 15
 DB 19 LASLSTFOQMWSKQ 33
 RESULT 3
 ABG08617
 ID ABG08617 standard; protein; 86 AA.
 XX
 AC ABG08617;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #8608.
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS72804.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 20; SEQ ID NO 38976; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 86 AA;

Query Match 100.0%; Score 75; DB 4; Length 86;
 Best Local Similarity 100.0%; Pred. No. 4e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFQQMWISQ 15
 |||||
 Db 57 LASLSTFQQMWISQ 71

RESULT 4
 ABP42928
 ID ABP42928 standard; protein; 110 AA.
 XX
 AC ABP42928;
 XX
 DT 22-AUG-2002 (first entry)
 XX
 DE Human ovarian antigen HPRS46, SEQ ID NO:4060.

XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive.

XX Homo sapiens.

XX WO200200677-A1.

XX 03-JAN-2002.

XX 07-JUN-2001; 2001WO-US018569.

XX 07-JUN-2000; 2000US-0209467P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Birse CE, Rosen CA;

XX WPI; 2002-147878/19.

XX N-PSDB; ABQ56005.

PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 PT cancer), immune disorders, cardiovascular disorders and neurological
 PT diseases.

XX Claim 11; SEQ ID NO 4060; 2922pp; English.

XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovary and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system

CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 110 AA;

Query Match 100.0%; Score 75; DB 5; Length 110;

Best Local Similarity 100.0%; Pred. No. 5.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFQQMWISQ 15
 |||||
 Db 81 LASLSTFQQMWISQ 95

RESULT 5

AAM81819

ID AAM81819 standard; protein; 129 AA.

XX AAM81819;

AC AAM81819;

DT 13-NOV-2001 (first entry)

XX Human haematological malignancy-related antigen #1517.

XX Human; cytostatic; vascular; gene therapy; vaccine; lymphoma;

XX haematological malignancy; antigen; chronic lymphocytic leukaemia;

XX follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.

XX Homo sapiens.

XX WO200164886-A2.

XX 07-SEP-2001.

XX 01-MAR-2001; 2001WO-US007272.

XX 01-MAR-2000; 2000US-0186126P.

XX 17-MAR-2000; 2000US-0190479P.

XX 27-APR-2000; 2000US-0200545P.

XX 28-APR-2000; 2000US-0200303P.

XX 28-APR-2000; 2000US-0200779P.

XX 01-MAY-2000; 2000US-0200999P.

XX 04-MAY-2000; 2000US-0202084P.

XX 14-JUL-2000; 2000US-0218950P.

XX 03-AUG-2000; 2000US-0222903P.

XX 04-AUG-2000; 2000US-0223416P.

XX 07-AUG-2000; 2000US-0223378P.

XX (CORI-) CORIXA CORP.

XX Gaiger A, Algate PA, Mannion J;

XX WPI; 2001-514842/56.

XX Compositions and methods for the detection of hematological malignancies,

PT e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and
 PT Hodgkin's and T/B cell non-Hodgkin's lymphoma.
 PS Claim 1; Page 1114; 1252pp; English.
 XX
 CC The present invention relates to compositions and methods for the
 CC detection, diagnosis and therapy of haematological malignancies. The
 CC present sequence is the protein sequence of a human haematological
 CC malignancy related antigen. The methods of the present invention comprise
 CC detecting the presence of haematological malignancy related antigen(s) in
 CC a sample obtained from the patient (an increased level of the
 CC polypeptide, compared to an unaffected individual, is indicative of an
 CC increased risk). Haematological malignancies which can be treated using
 CC the present invention are chronic lymphocytic leukaemia, lymphoma,
 CC follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B
 CC cell non-Hodgkin's lymphoma
 XX
 SQ Sequence 129 AA;

Query Match 100.0%; Score 75; DB 4; Length 129;
 Best Local Similarity 100.0%; Pred. No. 6.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFQQMWSKQ 15
 |||||
 Db 100 LASLSTFQQMWSKQ 114

RESULT 6
 AAU32061
 ID AAU32061 standard; protein; 135 AA.
 XX
 AC AAU32061;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secreted protein #2552.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 XX
 XX WO200179449-A2.
 PN
 XX
 PD 25-OCT-2001.
 XX
 XX 16-APR-2001; 2001WO-US008656.
 XX
 PF 18-APR-2000; 2000US-00552929.
 PR
 PR 26-JAN-2001; 2001US-00770160.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX
 XX Tang YT, Liu C, Drmanac RT;
 PI
 XX WPI; 2001-611725/70.
 DR
 XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy.
 XX
 XX Claim 20; Page 550; 765pp; English.

XX The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising the
 CC nucleic acids encoding the polypeptides and cells genetically engineered

CC to express them are also useful for producing the proteins. The proteins
 CC are useful in genetic vaccination, testing and therapy, and can be used
 CC as nutritional supplements. They may be used to increase stem cell
 CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
 CC and/or nerve tissue growth or regeneration; immune suppression and/or
 CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
 CC AAU29510-AAU33304 represent the amino acid sequences of novel human
 CC secreted proteins of the invention
 XX

SQ Sequence 135 AA;

Query Match 100.0%; Score 75; DB 4; Length 135;
 Best Local Similarity 100.0%; Pred. No. 6.5e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFQQMWSKQ 15
 |||||
 Db 97 LASLSTFQQMWSKQ 111

RESULT 7
 ABP43127
 ID ABP43127 standard; protein; 145 AA.
 XX
 AC ABP43127;
 XX

DT 22-AUG-2002 (first entry)

XX Human ovarian antigen HVBD91, SEQ ID NO:4259.

XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive.

XX Homo sapiens.

XX WO200200677-A1.

XX 03-JAN-2002.

XX 07-JUN-2001; 2001WO-US018569.

XX 07-JUN-2000; 2000US-0209467P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Birse CE, Rosen CA;

XX WPI; 2002-147878/19.

XX N-PSDB; ABQ56204.

XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 PT cancer), immune disorders, cardiovascular disorders and neurological
 PT diseases.

XX Claim 11; SEQ ID NO 4259; 2922pp; English.

XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovary and/or breast-related

disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 145 AA;

Query Match 100.0%; Score 75; DB 5; Length 145;
Best Local Similarity 100.0%; Pred. No. 7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LASLSTFQQMWSKQ 15
| | | | | | | | | | | | | | | | | |
Db 116 LASLSTFQQMWSKQ 130

RESULT 8
AAM80875
ID AAM80875 standard; protein; 147 AA.

AC AAM80875;

DT 13-NOV-2001 (first entry)

DE Human haematological malignancy-related antigen #573.

KW Human; cytostatic; vascular; gene therapy; vaccine; lymphoma;
KW haematological malignancy; antigen; chronic lymphocytic leukaemia;
KW follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.

XX Homo sapiens.

OS WO200164886-A2.

PN 07-SEP-2001.

PD 01-MAR-2001; 2001WO-US007272.

PF 01-MAR-2000; 2000US-0186126P.

PR 17-MAR-2000; 2000US-0190479P.

PR 27-APR-2000; 2000US-0200545P.

PR 28-APR-2000; 2000US-0200303P.

PR 01-MAY-2000; 2000US-0200779P.

PR 04-MAY-2000; 2000US-0200999P.

PR 14-JUL-2000; 2000US-0202084P.

PR 03-AUG-2000; 2000US-0222903P.

PR 07-AUG-2000; 2000US-0223416P.

XX (CORI-) CORIXA CORP.

XX Gaiger A, Algate PA, Mannion J;

XX WPI; 2001-514842/56.

XX Compositions and methods for the detection of hematological malignancies,
PT e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and
PT Hodgkin's and T/B cell non-Hodgkin's lymphoma.

PS Claim 1; Page 743-744; 1252pp; English.

XX The present invention relates to compositions and methods for the
CC detection, diagnosis and therapy of haematological malignancies. The
CC present sequence is the protein sequence of a human haematological
CC malignancy related antigen. The methods of the present invention comprise
CC detecting the presence of haematological malignancy related antigen(s) in
CC a sample obtained from the patient (an increased level of the
CC polypeptide, compared to an unaffected individual, is indicative of an
CC increased risk). Haematological malignancies which can be treated using
CC the present invention are chronic lymphocytic leukaemia, lymphoma,
CC follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B
CC cell non-Hodgkin's lymphoma

XX Sequence 147 AA;

Query Match 100.0%; Score 75; DB 4; Length 147;

Best Local Similarity 100.0%; Pred. No. 7.1e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LASLSTFQQMWSKQ 15
| | | | | | | | | | | | | | | | | |
Db 118 LASLSTFQQMWSKQ 132

RESULT 9

AAM81886
ID AAM81886 standard; protein; 147 AA.

AC AAM81886;

DT 13-NOV-2001 (first entry)

DE Human haematological malignancy-related antigen #1584.

XX Human; cytostatic; vascular; gene therapy; vaccine; lymphoma;
KW haematological malignancy; antigen; chronic lymphocytic leukaemia;
KW follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.

OS Homo sapiens.

XX WO200164886-A2.

PN 07-SEP-2001.

PD 01-MAR-2001; 2001WO-US007272.

PF 01-MAR-2000; 2000US-0186126P.

PR 17-MAR-2000; 2000US-0190479P.

PR 27-APR-2000; 2000US-0200545P.

PR 28-APR-2000; 2000US-0200303P.

PR 01-MAY-2000; 2000US-0200779P.

PR 04-MAY-2000; 2000US-0202084P.

PR 14-JUL-2000; 2000US-0206201P.

PR 03-AUG-2000; 2000US-0218950P.

PR 04-AUG-2000; 2000US-0222903P.

PR 07-AUG-2000; 2000US-0223416P.

XX (CORI-) CORIXA CORP.

XX Gaiger A, Algate PA, Mannion J;

XX WPI; 2001-514842/56.

XX Compositions and methods for the detection of hematological malignancies,
PT e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and

PT Hodgkin's and T/B cell non-Hodgkin's lymphoma.
 XX Claim 1; Page 1141; 1252pp; English.
 PS
 CC The present invention relates to compositions and methods for the
 CC detection, diagnosis and therapy of hematological malignancies. The
 CC present sequence is the protein sequence of a human haematological
 CC malignancy related antigen. The methods of the present invention comprise
 CC detecting the presence of hematological malignancy related antigen(s) in
 CC a sample obtained from the patient (an increased level of the
 CC polypeptide, compared to an unaffected individual, is indicative of an
 CC increased risk). Haematological malignancies which can be treated using
 CC the present invention are chronic lymphocytic leukaemia, lymphoma,
 CC follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B
 CC cell non-Hodgkin's lymphoma
 XX
 SQ Sequence 147 AA;
 Query Match 100.0%; Score 75; DB 4; Length 147;
 Best Local Similarity 100.0%; Pred. No. 7.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LASLSTFQQMWISKQ 15
 |||||
 DB 118 LASLSTFQQMWISKQ 132
 |||||
 RESULT 10
 AAM81332
 ID AAM81332 standard; protein; 147 AA.
 AC
 XX AAM81332;
 DT
 DT 13-NOV-2001 (first entry)
 XX
 DE Human haematological malignancy-related antigen #1030.
 XX
 KW Human; cytostatic; vascular; gene therapy; vaccine; lymphoma;
 KW haematological malignancy; antigen; chronic lymphocytic leukaemia;
 KW follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.
 XX
 OS Homo sapiens.
 XX
 XX WO200164886-A2.
 XX
 XX 07-SEP-2001.
 XX
 XX 01-MAR-2001; 2001WO-US007272.
 XX
 PR 01-MAR-2000; 2000US-0186126P.
 PR 17-MAR-2000; 2000US-0190479P.
 PR 27-APR-2000; 2000US-0200545P.
 PR 28-APR-2000; 2000US-0200303P.
 PR 28-APR-2000; 2000US-0200779P.
 PR 01-MAY-2000; 2000US-0200999P.
 PR 04-MAY-2000; 2000US-0202084P.
 PR 14-MAY-2000; 2000US-0206201P.
 PR 03-AUG-2000; 2000US-0218950P.
 PR 04-AUG-2000; 2000US-0222903P.
 PR 07-AUG-2000; 2000US-0223416P.
 XX
 XX (CORI-) CORIXA CORP.
 XX
 XX Gaiger A, Algate PA, Mannion J;
 PI
 XX WPI; 2001-514842/56.
 DR
 XX Compositions and methods for the detection of hematological malignancies,
 PT e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and
 PT Hodgkin's and T/B cell non-Hodgkin's lymphoma.
 XX
 PS Claim 1; Page 925; 1252pp; English.

XX
 CC The present invention relates to compositions and methods for the
 CC detection, diagnosis and therapy of haematological malignancies. The
 CC present sequence is the protein sequence of a human haematological
 CC malignancy related antigen. The methods of the present invention comprise
 CC detecting the presence of hematological malignancy related antigen(s) in
 CC a sample obtained from the patient (an increased level of the
 CC polypeptide, compared to an unaffected individual, is indicative of an
 CC increased risk). Haematological malignancies which can be treated using
 CC the present invention are chronic lymphocytic leukaemia, lymphoma,
 CC follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B
 CC cell non-Hodgkin's lymphoma
 XX
 SQ Sequence 147 AA;
 Query Match 100.0%; Score 75; DB 4; Length 147;
 Best Local Similarity 100.0%; Pred. No. 7.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LASLSTFQQMWISKQ 15
 |||||
 DB 118 LASLSTFQQMWISKQ 132
 |||||
 RESULT 11
 ABO84771
 ID ABO84771 standard; protein; 149 AA.
 AC
 XX ABO84771;
 DT
 DT 18-NOV-2004 (first entry)
 XX
 DE Human cancer-associated protein (CAP) HP07-010.
 KW Human; cancer-associated protein; CAP; cancer; cytostatic.
 XX
 OS Homo sapiens.
 XX
 XX WO2004058146-A2.
 XX
 XX 15-JUL-2004.
 XX
 XX 15-DEC-2003; 2003WO-US040081.
 XX
 XX 17-DEC-2002; 2002US-00322281.
 XX
 XX (SAGR-) SAGRES DISCOVERY INC.
 XX
 XX Morris DW, Malandro MS;
 PI
 XX WPI; 2004-499109/47.
 XX N-PSDB; ABD3111.
 XX
 XX Novel human cancer associated protein encoded within open reading frame
 XX of cancer associated gene, useful as targets for diagnosing cancer.
 XX
 XX Claim 18; SEQ ID NO 66; 182pp; English.
 XX
 XX The invention relates to cancer-associated proteins (CAP) and the cancer-
 XX associated (CA) nucleic acids encoding them. The invention also relates
 XX to a method for treating cancers involving administering to a patient an
 XX inhibitor of CAP, and a method of screening for anticancer activity in a
 XX potential drug involving providing a cell that expresses a CA gene,
 XX contacting a tissue sample derived from a cancer cell with an anticancer
 XX drug candidate and monitoring the effect of the anticancer drug candidate
 XX on expression of the CA gene. The CAP proteins are useful for detecting
 XX cancer associated with expression of a CAP protein in a test cell sample
 XX and for screening for a bioactive agent capable of modulating the
 XX activity of a CAP protein. The CA nucleic acids are useful for diagnosing
 XX cancer, involving determining the expression of a CA nucleic acid in a
 XX tissue. This sequence represents a human CAP of the invention. Note: The
 XX sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic format directly from WIPO

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CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 149 AA;
    Query Match      100.0%; Score 75; DB 8; Length 149;
    Best Local Similarity 100.0%; Pred. No. 7.2e-05;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LASLSTFOQMWSKQ 15
Db 120 LASLSTFOQMWSKQ 134
    RESULT 12
    ABG11441
    ID ABG11441 standard; protein; 181 AA.
    XX
    AC ABG11441;
    DT
    DE 18-FEB-2002 (first entry)
    DE Novel human diagnostic protein #11432.
    XX
    KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
    KW food supplement; medical imaging; diagnostic; genetic disorder.
    XX
    OS Homo sapiens.
    XX
    PN WO200175067-A2.
    XX
    PD 11-OCT-2001.
    XX
    PF 30-MAR-2001; 2001WO-US008631.
    XX
    PR 31-MAR-2000; 2000US-00540217.
    PR 23-AUG-2000; 2000US-00649167.
    XX
    PA (HYSE-) HYSEQ INC.
    XX
    PI Dmanac RT, Liu C, Tang YT;
    XX
    DR WPI; 2001-639362/73.
    DR N-PSDB; AAS75628.
    XX
    PT New isolated polynucleotide and encoded polypeptides, useful in
    PT diagnostics, forensics, gene mapping, identification of mutations
    PT responsible for genetic disorders or other traits and to assess
    PT biodiversity.
    XX
    PS Claim 20; SEQ ID NO 41800; 103pp; English.
    XX
    CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
    CC sequences. (I) is useful as hybridisation probes, polymerase chain
    CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
    CC and in recombinant production of (II). The polynucleotides are also used
    CC in diagnostics as expressed sequence tags for identifying expressed
    CC genes. (II) is useful in gene therapy techniques to restore normal
    CC activity of (II) or to treat disease states involving (II). (II) is
    CC useful for generating antibodies against it, detecting or quantitating a
    CC polypeptide in tissue, as molecular weight markers and as a food
    CC supplement. (II) and its binding partners are useful in medical imaging
    CC of sites expressing (II). (I) and (II) are useful for treating disorders
    CC involving aberrant protein expression or biological activity. The
    CC polypeptide and polynucleotide sequences have applications in
    CC diagnostics, forensics, gene mapping, identification of mutations
    CC responsible for genetic disorders or other traits to assess biodiversity
    CC and to produce other types of data and products dependent on DNA and
    CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
    CC amino acid sequences of the invention. Note: The sequence data for this
    CC patent did not appear in the printed specification, but was obtained in
    CC electronic format directly from WIPO at
    CC ftp.wipo.int/pub/published_pct_sequences
    XX

SQ Sequence 181 AA;
    Query Match      100.0%; Score 75; DB 4; Length 181;
    Best Local Similarity 100.0%; Pred. No. 8.8e-05;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LASLSTFOQMWSKQ 15
Db 152 LASLSTFOQMWSKQ 166
    RESULT 13
    ADA55146
    ID ADA55146 standard; protein; 197 AA.
    XX
    AC ADA55146;
    DT
    DE 20-NOV-2003 (first entry)
    DE Human protein, SEQ ID 2714.
    XX
    KW Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
    KW Gene therapy; human; secretory protein; membrane proteins; cancer;
    KW inflammatory disease; osteoporosis; neurological disease.
    XX
    OS Homo sapiens.
    XX
    PN EP1293569-A2.
    XX
    PD 19-MAR-2003.
    XX
    PF 21-MAR-2002; 2002EP-00006586.
    XX
    PR 14-SEP-2001; 2001JP-00328381.
    PR 24-JAN-2002; 2002US-0350435P.
    XX
    PA (HELI-) HELIX RES INST.
    PA (REAS-) RES ASSOC BIOTECHNOLOGY.
    XX
    PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
    PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
    PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
    XX
    DR WPI; 2003-395539/38.
    DR N-PSDB; ADA53507.
    XX
    PT New polynucleotides encoding full-length polypeptides, e.g. secretory
    PT and/or membrane proteins, useful for developing medicines for diseases in
    PT which the gene is involved, or as target molecules for gene therapy.
    XX
    PS Claim 14; SEQ ID NO 2714; 205pp; English.
    XX
    CC The present invention relates to novel human secretory or membrane
    CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
    CC ADA54071). The coding sequences are useful in the gene therapy of
    CC diseases caused by abnormalities of the proteins, e.g. cancer,
    CC inflammatory diseases, osteoporosis or neurological disease.
    XX
    PS Sequence 197 AA;
    Query Match      100.0%; Score 75; DB 6; Length 197;
    Best Local Similarity 100.0%; Pred. No. 9.6e-05;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LASLSTFOQMWSKQ 15
Db 168 LASLSTFOQMWSKQ 182
    RESULT 14
    ABG08618
    ID ABG08618 standard; protein; 250 AA.
    XX
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AC ABG08618;
 XX 13-FEB-2002 (first entry)
 XX Novel human diagnostic protein #8609.
 DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
 XX food supplement; medical imaging; diagnostic; genetic disorder.
 KW Homo sapiens.
 XX WO200175067-A2.
 XX 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US008631.
 XX 31-MAR-2000; 2000US-00540217.
 XX 23-AUG-2000; 2000US-00649167.
 XX (HYSE-) HYSEQ INC.
 XX Drmanac RT, Liu C, Tang YT;
 XX N-PSDB; AAS72805.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX Claim 20; SEQ ID NO 38977; 103pp; English.
 PS The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (II) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 250 AA;
 SQ Query Match 100.0%; Score 75; DB 4; Length 250;
 Best Local Similarity 100.0%; Pred. No. 0.00012;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LASLSTFQQMWISKQ 15
 Db 220 LASLSTFQQMWISKQ 234
 RESULT 15
 ABU70549
 ID ABU70549 standard; protein; 274 AA.
 XX AC ABU70549;
 XX

DT 10-JUN-2003 (first entry)
 XX Human adipocyte Selected Interacting domain, SID, #180.
 DE Human; prey; adipocyte; SID; selected interacting domain; anorectic;
 XX antidiabetic; protein-protein interaction; diabetes;
 KW Yeast 2-hybrid assay; metabolic disorder; obesity.
 XX Homo sapiens.
 OS WO200286122-A2.
 XX 31-OCT-2002.
 XX 14-MAR-2002; 2002WO-EP003768.
 XX 14-MAR-2001; 2001US-0275734P.
 XX (HYBR-) HYBRIGENICS.
 XX Legrain P, Daviet L;
 XX WPI; 2003-103412/09.
 XX N-PSDB; ACAS7093.
 XX New complex between two interacting proteins in adipocyte cells, useful
 PT for identifying selected interacting domains that modulate protein
 PT interactions, or for preventing or treating metabolic disorders such as
 XX obesity or diabetes.
 XX Claim 6; Page 167; 382pp; English.
 PS The invention relates to a complex between two interacting proteins in
 CC adipocyte cells, given in the specification. The proteins are identified
 CC by selecting a bait protein from a known adipocyte marker and then
 CC performing a yeast 2-hybrid selection to isolate prey proteins encoded by
 CC members of an adipocyte cDNA library. The proteins are designated SID
 CC (RTM) (selected interacting domains) proteins. Also included are a
 CC polynucleotide encoding a polypeptide in the adipocyte cells, a
 CC recombinant host cell expressing at least one of the interacting
 CC polypeptides of the complex, selecting a modulating compound in adipocyte
 CC cells, a SID (RTM) polypeptide comprising any of the 738 amino acid
 CC sequences given in the specification (including its fragment or variant),
 CC a SID (RTM) polynucleotide comprising any of the 738 nucleotide sequences
 CC given in the specification (including its fragment or variant), a vector
 CC comprising the SID (RTM) polynucleotide, a recombinant host cell
 CC comprising the vector, a protein chip comprising the polypeptides and a
 CC record comprising all or part of the data, listed in the specification.
 CC The complex, polypeptides, polynucleotides and compounds are useful for
 CC preventing or treating metabolic disorders such as obesity or diabetes.
 CC The polynucleotides are useful as probes or primers. The complex is
 CC particularly useful for identifying selected interacting domains (SID
 CC (RTM)) for screening drugs that modulate the protein interaction, thus
 CC exhibiting the therapeutic effect. The present sequence represents a SID
 CC (prey) protein of the invention
 XX Sequence 274 AA;
 SQ Query Match 100.0%; Score 75; DB 6; Length 274;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LASLSTFQQMWISKQ 15
 Db 245 LASLSTFQQMWISKQ 259
 Search completed: April 8, 2005, 10:50:47
 Job time : 63.4 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:57; Search time 17.5333 Seconds
(without alignments)
63.863 Million cell updates/sec

Title: US-09-423-351C-8

Perfect score: 75

Sequence: 1 LASLSTFQWMWISKQ 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	100.0	239	4	US-09-949-016-10409
2	75	100.0	374	3	US-08-609-236-6
3	75	100.0	375	3	US-09-106-217-16
4	75	100.0	375	3	US-09-171-337A-7
5	75	100.0	375	4	US-09-631-022-7
6	75	100.0	375	4	US-09-976-594-731
7	75	100.0	377	3	US-09-106-217-2
8	75	100.0	377	4	US-09-919-172-33
9	75	100.0	377	4	US-09-917-254-53
10	75	100.0	377	4	US-09-248-796A-14109
11	75	100.0	386	4	US-09-949-016-7721
12	75	100.0	399	4	US-09-949-016-9424
13	75	100.0	404	4	US-09-949-016-11313
14	70	93.3	23	4	US-09-700-436-4
15	70	93.3	375	2	US-08-494-151-14
16	70	93.3	375	3	US-09-171-337A-8
17	70	93.3	375	4	US-09-631-022-8
18	70	93.3	376	1	US-08-588-113-2
19	70	93.3	376	4	US-09-949-016-6100
20	70	93.3	402	4	US-09-949-016-10757
21	65	86.7	47	3	US-09-306-446C-7
22	65	86.7	374	3	US-09-306-446C-2
23	64	85.3	164	4	US-09-270-767-33348
24	64	85.3	164	4	US-09-270-767-48565
25	58	77.3	362	4	US-09-949-016-7725
26	58	77.3	376	4	US-09-538-092-1109
27	58	77.3	376	4	US-09-538-092-1110

28	77.3	376	4	US-09-949-016-6656	Sequence 6656, Ap	
29	58	77.3	376	4	US-09-949-016-8452	Sequence 8452, Ap
30	51	68.0	336	4	US-09-248-796A-14108	Sequence 14108, A
31	47	62.7	497	4	US-09-248-796A-18965	Sequence 18965, A
32	46	61.3	384	4	US-09-538-092-395	Sequence 395, App
33	41	54.7	313	4	US-09-198-452A-794	Sequence 794, App
34	41	54.7	333	4	US-09-438-185A-746	Sequence 746, App
35	40	53.3	1805	4	US-09-949-016-8246	Sequence 8246, App
36	39	52.0	161	4	US-09-270-767-40150	Sequence 40150, A
37	39	52.0	161	4	US-09-270-767-55366	Sequence 55366, A
38	39	52.0	419	4	US-09-328-352-6451	Sequence 6451, Ap
39	39	52.0	460	4	US-09-489-039A-13505	Sequence 13505, A
40	38	50.7	73	4	US-09-621-976-6616	Sequence 6616, Ap
41	38	50.7	84	4	US-09-328-352-4655	Sequence 4655, Ap
42	38	50.7	300	4	US-09-252-991A-26038	Sequence 26038, A
43	38	50.7	347	4	US-09-543-681A-6024	Sequence 6024, Ap
44	38	50.7	603	4	US-09-396-149-8	Sequence 8, Appli
45	38	50.7	940	4	US-09-328-352-8165	Sequence 8165, Ap

ALIGNMENTS

RESULT 1
US-09-949-016-10409
; Sequence 10409, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10409
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10409

Query Match 100.0%; Score 75; DB 4; Length 239;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFQWMWISKQ 15
Db 210 LASLSTFQWMWISKQ 224

RESULT 2
US-08-609-236-6
; Sequence 6, Application US/08609236
; Patent No. 6087398
; GENERAL INFORMATION:
; APPLICANT: Steven R. Goodman
; TITLE OF INVENTION: No. 6087398el Sickle Cell Anemia Treatment
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McGregor & Adler, LLP
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,236
; FILING DATE: March 1, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/002,288
; FILING DATE: August 14, 1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Benjamin Aaron Adler, Ph.D.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5807
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6908
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374
; TYPE: Amino acid
; STRANDEDNESS:
; TOPOLOGY: Linear
; MOLECULE TYPE: Protein
; DESCRIPTION: Protein
; HYPOTHETICAL: NO
; ANTI-SENSE: No
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; CELL LINE:
; US-08-609-236-6

Query Match 100.0%; Score 75; DB 3; Length 374;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFQQMWISKQ 15
Db 345 LASLSTFQQMWISKQ 359

RESULT 3
US-09-106-217-16
; Sequence 16, Application US/09106217
; Patent No. 6063576
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Olson, Timothy M.
; TITLE OF INVENTION: Actin Mutations in Dilated
; TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; STREET: Tower
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,217

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; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 2323-125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-106-217-16

Query Match 100.0%; Score 75; DB 3; Length 375;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFQQMWISKQ 15
Db 346 LASLSTFQQMWISKQ 360

RESULT 4
US-09-171-337A-7
; Sequence 7, Application US/09171337A
; Patent No. 6300095
; GENERAL INFORMATION:
; APPLICANT: BARREDO FUENTE, Jose Luis
; RODRIGUEZ SAIZ, Marta
; COLLADOS DE LA VIEJA, Alfonso J.
; MORENO VALLE, Migueal Angel
; SALTO MALDONADO, Francisco
; DIEZ GARCIA, Bruno
; TITLE OF INVENTION: PROMOTERS OF THE GENES GLUTAMATE
; DESHYDROGENASE, -N-ACETYLHEXOSAMINIDASE
; AND -ACTIN AND THEIR USE IN FILAMENTOUS
; FUNGI EXPRESSION, SECRETION AND ANTISENSE
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LADAS & PARRY
; STREET: 26 WEST 61 STREET
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3-1/4" Disk 1.44MB
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11
; SOFTWARE: Wordperfect 8 for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/171,337A
; FILING DATE: 14-May-1999
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/ES98/00056
; FILING DATE: 5-MAR-1998
; APPLICATION NUMBER: ES9700482
; FILING DATE: 5-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: MASS, Clifford J.
; REGISTRATION NUMBER: 30,086
; (C) REF./DOCKET NO.: U-011948-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 233288
; INFORMATION FOR SEQ ID NO: 7
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acids

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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE: Penicillium chrysogenum
FEATURE: amino acid sequence of the -actin
protein with a molecular weight of 41760 Da.
SEQUENCE DESCRIPTION: SEQ ID NO: 7

US-09-171-337A-7
Query Match 100.0%; Score 75; DB 3; Length 375;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFOQMWSKQ 15
Db 346 LASLSTFOQMWSKQ 360

RESULT 5

US-09-631-022-7
; Sequence 7, Application US/09631022
; Patent No. 6558921
; GENERAL INFORMATION:
; APPLICANT: BARREDO FUENTE, Jose Luis
; RODRIGUEZ SAIZ, Marta
; COLLADOS DE LA VIEJA, Alfonso J.
; MORENO VALLE, Migueu Angel
; SALTO MALDONADO, Francisco
; DIEZ GARCIA, Bruno
; TITLE OF INVENTION: PROMOTERS OF THE GENES GLUTAMATE
; DESHYDROGENASE, -N-ACETYLHEXOSAMINIDASE
; AND -ACTIN AND THEIR USE IN FILAMENTOUS
; FUNGI EXPRESSION, SECRETION AND ANTISENSE

NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: LADAS & PARRY
STREET: 26 WEST 61 STREET
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10023

COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/4" Disk 1.44MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11
SOFTWARE: WordPerfect 8 for Windows

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/631,022
FILING DATE: 02-Aug-2000

CLASSIFICATION DATA:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/171,337
FILING DATE: 14-MAY-1999

APPLICATION NUMBER: PCT/ES98/00056
FILING DATE: 5-MAR-1998
APPLICATION NUMBER: ES9700482
FILING DATE: 5-MAR-1997

ATTORNEY/AGENT INFORMATION:
NAME: MASS, Clifford J.
REGISTRATION NUMBER: 30,086

TELECOMMUNICATION INFORMATION:
TELEPHONE: 233288
INFORMATION FOR SEQ ID NO: 7

SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acids

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

ORIGINAL SOURCE:
ORGANISM: Penicillium chrysogenum
FEATURE: amino acid sequence of the -actin
protein with a molecular weight of 41760 Da.
SEQUENCE DESCRIPTION: SEQ ID NO: 7

US-09-631-022-7
Query Match 100.0%; Score 75; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFOQMWSKQ 15
Db 346 LASLSTFOQMWSKQ 360

RESULT 6

US-09-976-594-731
; Sequence 731, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 731
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1837317CD1
US-09-976-594-731

Query Match 100.0%; Score 75; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFOQMWSKQ 15
Db 346 LASLSTFOQMWSKQ 360

RESULT 7

US-09-106-217-2
; Sequence 2, Application US/09106217
; Patent No. 6063576
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Olson, Timothy M.
; TITLE OF INVENTION: Actin Mutations in Dilated
; TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; STREET: Tower
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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US-09-949-016-7721
; Sequence 7721, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOW
; TITLE OF INVENTION: WITH HUMAN DISEASE,
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7721
; LENGTH: 386
; TYPE: prt
; ORGANISM: Human

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US-09-949-016-7721

Query Match 100.0%; Score 75; DB 4; Length 386;
Best Local Similarity 100.0%; Pred. No. 4.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASLSTFOQMWSKQ 15
| | | | | | | | | | | | | | | | | |
DB 357 LASLSTFOQMWSKQ 371

RESULT 12

US-09-949-016-9424
; Sequence 9424, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9424
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9424

Query Match 100.0%; Score 75; DB 4; Length 399;
Best Local Similarity 100.0%; Pred. No. 4.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASLSTFOQMWSKQ 15
| | | | | | | | | | | | | | | | | |
DB 370 LASLSTFOQMWSKQ 384

RESULT 13

US-09-949-016-11313
; Sequence 11313, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11313
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11313

Query Match 100.0%; Score 75; DB 4; Length 404;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASLSTFOQMWSKQ 15
| | | | | | | | | | | | | | | | | |
DB 375 LASLSTFOQMWSKQ 389

RESULT 14

US-09-700-436-4
; Sequence 4, Application US/09700436
; Patent No. 6482802
; GENERAL INFORMATION:
; APPLICANT: Hu, Guo-Fu
; APPLICANT: Vallee, Burt L.
; TITLE OF INVENTION: USE OF NEOMYCIN FOR TREATING
; ANGIOGENESIS RELATED DISEASES
; FILE REFERENCE: 9457-008-999
; CURRENT APPLICATION NUMBER: US/09/700,436
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: PCT/US99/10269
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/084,921
; PRIOR FILING DATE: 1998-05-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-700-436-4

Query Match 93.3%; Score 70; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASLSTFOQMWSK 14
| | | | | | | | | | | | | | | | | |
DB 10 LASLSTFOQMWSK 23

RESULT 15

US-08-494-151-14
; Sequence 14, Application US/08494151
; Patent No. 5840528
; GENERAL INFORMATION:
; APPLICANT: Van Ooyen, Albert Johannes Joseph
; TITLE OF INVENTION: Transformation of Phaffia rhodozyma
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/494,151
; FILING DATE: 23-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20039.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-494-151-14

Query Match 93.3%; Score 70; DB 2; Length 375;
Best Local Similarity 93.3%; Pred. No. 0.00031;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LASLSTFQOMWISKQ 15
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Db 346 LASLSTFQOMWISKQ 360

Search completed: April 8, 2005, 12:07:37
Job time : 18.5333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 10:53:18 ; Search time 42.6667 Seconds
(without alignments)
116.718 Million cell updates/sec

Title: US-09-423-351C-8

Perfect score: 75
Sequence: 1 LASLSTFOQMWISKQ 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 331997259 residues

Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
 - 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
 - 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
 - 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	75	100.0	47	15 US-10-341-434-139	Sequence 139, App
2	75	100.0	74	16 US-10-767-701-33598	Sequence 33598, A
3	75	100.0	81	15 US-10-424-599-157586	Sequence 157586, A
4	75	100.0	95	16 US-10-767-701-55472	Sequence 55472, A
5	75	100.0	110	15 US-10-284-049-4060	Sequence 4060, App
6	75	100.0	129	9 US-09-796-692-2183	Sequence 2183, App
7	75	100.0	129	14 US-10-040-862-2183	Sequence 2183, App
8	75	100.0	129	15 US-10-057-475B-2183	Sequence 2183, App
9	75	100.0	129	15 US-10-154-884B-2183	Sequence 2183, App
10	75	100.0	129	16 US-10-764-324-2183	Sequence 2183, App
11	75	100.0	133	15 US-10-424-599-143033	Sequence 143033, App
12	75	100.0	145	15 US-10-264-049-4259	Sequence 4259, App
13	75	100.0	147	9 US-09-796-692-1239	Sequence 1239, App

14	75	100.0	147	9 US-09-796-692-1696	Sequence 1696, App
15	75	100.0	147	9 US-09-796-692-2250	Sequence 2250, App
16	75	100.0	147	14 US-10-040-862-1239	Sequence 1239, App
17	75	100.0	147	14 US-10-040-862-1696	Sequence 1696, App
18	75	100.0	147	14 US-10-040-862-2250	Sequence 2250, App
19	75	100.0	147	15 US-10-057-475B-1239	Sequence 1239, App
20	75	100.0	147	15 US-10-057-475B-1696	Sequence 1696, App
21	75	100.0	147	15 US-10-057-475B-2250	Sequence 2250, App
22	75	100.0	147	15 US-10-154-884B-1239	Sequence 1239, App
23	75	100.0	147	15 US-10-154-884B-1696	Sequence 1696, App
24	75	100.0	147	15 US-10-154-884B-2250	Sequence 2250, App
25	75	100.0	147	16 US-10-322-281-66	Sequence 66, Appl
26	75	100.0	147	16 US-10-764-324-1239	Sequence 1239, App
27	75	100.0	147	16 US-10-764-324-1696	Sequence 1696, App
28	75	100.0	147	16 US-10-764-324-2250	Sequence 2250, App
29	75	100.0	197	15 US-10-094-749-2714	Sequence 2714, App
30	75	100.0	371	16 US-10-322-281-68	Sequence 68, Appl
31	75	100.0	375	14 US-10-205-194-93	Sequence 93, Appl
32	75	100.0	375	14 US-10-316-253-88	Sequence 88, Appl
33	75	100.0	375	15 US-10-369-493-2436	Sequence 2436, App
34	75	100.0	375	15 US-10-369-493-5927	Sequence 5927, App
35	75	100.0	375	15 US-10-205-331-94	Sequence 94, Appl
36	75	100.0	375	15 US-10-260-708-82	Sequence 82, Appl
37	75	100.0	377	9 US-09-919-172-33	Sequence 33, Appl
38	75	100.0	377	15 US-10-236-031B-64	Sequence 64, Appl
39	75	100.0	378	15 US-10-369-493-12372	Sequence 12372, A
40	75	100.0	393	15 US-10-092-900A-310	Sequence 310, App
41	75	100.0	398	16 US-10-322-281-63	Sequence 63, Appl
42	75	100.0	413	9 US-09-925-301-1436	Sequence 1436, App
43	75	100.0	448	15 US-10-369-493-4105	Sequence 4105, App
44	75	100.0	883	15 US-10-112-944-715	Sequence 715, App
45	72	96.0	38	16 US-10-767-701-47237	Sequence 47237, A

ALIGNMENTS

RESULT 1
US-10-341-434-139
; Sequence 139, Application US/10341434
; Publication No. US20030215835A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
; FILE REFERENCE: 9U 204 205 R1
; CURRENT APPLICATION NUMBER: US/10/341,434
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/348,164
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 60/348,119
; PRIOR FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 139
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-341-434-139

Query Match 100.0%; Score 75; DB 15; Length 47;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LASLSTFOQMWISKQ 15

DB 18 LASLSTFOQMWISKQ 32

RESULT 2

US-10-767-701-33598
; Sequence 33598, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:

; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 33598
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C33956_1.pep
US-10-767-701-33598

Query Match 100.0%; Score 75; DB 16; Length 74;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFQQMWISKQ 15
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Db 45 LASLSTFQQMWISKQ 59

RESULT 3
US-10-424-599-157586
; Sequence 157586, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 157586
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_11331C.1.pep
US-10-424-599-157586

Query Match 100.0%; Score 75; DB 15; Length 81;
Best Local Similarity 100.0%; Pred. No. 4.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFQQMWISKQ 15
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Db 52 LASLSTFQQMWISKQ 66

RESULT 4
US-10-767-701-55472
; Sequence 55472, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 55472

; LENGTH: 95
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 30163357.pep
US-10-767-701-55472

Query Match 100.0%; Score 75; DB 16; Length 95;
Best Local Similarity 100.0%; Pred. No. 5.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFQQMWISKQ 15
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Db 66 LASLSTFQQMWISKQ 80

RESULT 5
US-10-264-049-4060
; Sequence 4060, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4060
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-4060

Query Match 100.0%; Score 75; DB 15; Length 110;
Best Local Similarity 100.0%; Pred. No. 6.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFQQMWISKQ 15
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RESULT 6
US-09-796-692-2183
; Sequence 2183, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077,001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084


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; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2183
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variant
; LOCATION: (1)...(129)
; OTHER INFORMATION: Xaa = Any amino acid
US-09-796-692-2183
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Query Match 100.0%; Score 75; DB 9; Length 129;
Best Local Similarity 100.0%; Pred. No. 7.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 LASLSTFOQMWSKQ 15
Db 100 LASLSTFOQMWSKQ 114
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RESULT 7

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; Sequence 2183, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2183
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variant
; LOCATION: (1)...(129)
; OTHER INFORMATION: Xaa = Any amino acid
US-10-057-475B-2183
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2183
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variant
; LOCATION: (1)...(129)
; OTHER INFORMATION: Xaa = Any amino acid
US-10-040-862-2183
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Best Local Similarity 100.0%; Pred. No. 7.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 LASLSTFOQMWSKQ 15
Db 100 LASLSTFOQMWSKQ 114
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RESULT 8

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US-10-057-475B-2183
; Sequence 2183, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2183
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variant
; LOCATION: (1)...(129)
; OTHER INFORMATION: Xaa = Any amino acid
US-10-057-475B-2183
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Best Local Similarity 100.0%; Pred. No. 7.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFQQMWISKQ 15
Db 100 LASLSTFQQMWISKQ 114

RESULT 9
US-10-154-884B-2183
; Sequence 2183, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-01352105
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2183
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variant
; LOCATION: (1)...(129)
; OTHER INFORMATION: Xaa = Any amino acid
US-10-154-884B-2183

Query Match      100.0%; Score 75; DB 15; Length 129;
Best Local Similarity 100.0%; Pred. No. 7.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 100 LASLSTFQQMWISKQ 114

RESULT 10
US-10-764-324-2183
; Sequence 2183, Application US/10764324
; Publication No. US20040175739A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-01352005
; CURRENT APPLICATION NUMBER: US/10/764,324
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2183
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variant
; LOCATION: (1)...(129)
; OTHER INFORMATION: Xaa = Any amino acid
US-10-154-884B-2183

Query Match      100.0%; Score 75; DB 15; Length 129;
Best Local Similarity 100.0%; Pred. No. 7.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LASLSTFQQMWISKQ 15
Db 100 LASLSTFQQMWISKQ 114

RESULT 11
US-10-424-599-143033
; Sequence 143033, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 143033
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_100172C.1.pep
US-10-424-599-143033
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Query Match      100.0%; Score 75; DB 15; Length 133;
Best Local Similarity 100.0%; Pred. No. 7.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LASLSTFOQMWSKQ 15
Db      104 LASLSTFOQMWSKQ 118

RESULT 12
US-10-264-049-4259
; Sequence 4259, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4259
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MISC_FEATURE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-4259

Query Match      100.0%; Score 75; DB 15; Length 145;
Best Local Similarity 100.0%; Pred. No. 8.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LASLSTFOQMWSKQ 15
Db      116 LASLSTFOQMWSKQ 130

RESULT 13
US-09-796-692-1239
; Sequence 1239, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1696
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-692-1239

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; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1239
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-692-1239

Query Match      100.0%; Score 75; DB 9; Length 147;
Best Local Similarity 100.0%; Pred. No. 8.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LASLSTFOQMWSKQ 15
Db      118 LASLSTFOQMWSKQ 132

RESULT 14
US-09-796-692-1696
; Sequence 1696, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1696
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-692-1696

Query Match      100.0%; Score 75; DB 9; Length 147;
Best Local Similarity 100.0%; Pred. No. 8.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 LASLSTFQQMWISKQ 15
Db 118 LASLSTFQQMWISKQ 132

RESULT 15
US-09-796-692-2250
; Sequence 2250, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: PAST-SEQ for Windows Version 3.0
; SEQ ID NO 2250
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-692-2250

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Query Match      100.0%; Score 75; DB 9; Length 147;
Best Local Similarity 100.0%; Pred. No. 8.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 LASLSTFQQMWISKQ 15
|||
Db 118 LASLSTFQQMWISKQ 132

Search completed: April 8, 2005, 12:51:00
Job time : 43.6667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:57 ; Search time 17.5333 Seconds
(without alignments)
63.863 Million cell updates/sec

Title: US-09-423-351C-1
Perfect score: 80
Sequence: 1 APRAVFSPSIVGRPRH 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PTCUS_COMB.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	80	100.0	71	4	US-09-621-976-6521
2	80	100.0	374	3	US-08-609-236-6
3	80	100.0	375	2	US-08-494-151-14
4	80	100.0	375	3	US-09-106-217-16
5	80	100.0	375	3	US-09-171-337A-7
6	80	100.0	375	3	US-09-171-337A-8
7	80	100.0	375	4	US-09-631-022-7
8	80	100.0	375	4	US-09-631-022-8
9	80	100.0	375	4	US-09-976-594-731
10	80	100.0	376	1	US-08-588-113-2
11	80	100.0	376	4	US-09-949-016-6100
12	80	100.0	377	3	US-09-106-217-2
13	80	100.0	377	4	US-09-919-172-33
14	80	100.0	377	4	US-09-917-254-53
15	80	100.0	386	4	US-09-949-016-7721
16	80	100.0	399	4	US-09-949-016-9424
17	80	100.0	402	4	US-09-949-016-10757
18	80	100.0	404	4	US-09-949-016-11313
19	78	97.5	377	4	US-09-248-796A-14109
20	74	92.5	41	3	US-09-306-446C-3
21	74	92.5	374	3	US-09-306-446C-2
22	56	70.0	11	4	US-09-786-066-5
23	51	63.7	362	4	US-09-949-016-7725
24	51	63.7	376	4	US-09-538-092-1109
25	51	63.7	376	4	US-09-538-092-1110
26	51	63.7	376	4	US-09-949-016-6656
27	51	63.7	376	4	US-09-949-016-8452

28	50	62.5	20	3	US-08-505-250-17	Sequence 17, Appl
29	50	62.5	20	3	US-08-505-250-17	Sequence 17, Appl
30	50	62.5	504	4	US-09-554-726A-10	Sequence 10, Appl
31	46	57.5	394	4	US-09-949-016-6655	Sequence 6655, Ap
32	46	57.5	406	4	US-09-949-016-7396	Sequence 7396, Ap
33	44	55.0	9	4	US-09-786-066-3	Sequence 3, Appl
34	43	53.8	374	4	US-09-252-991A-28830	Sequence 28830, A
35	42	52.5	1387	4	US-09-902-540-11948	Sequence 11948, A
36	42	52.5	2142	4	US-09-538-092-1142	Sequence 1142, A
37	41	51.2	538	4	US-09-252-991A-25373	Sequence 25373, A
38	40	50.0	78	4	US-09-621-976-5181	Sequence 5181, Ap
39	40	50.0	252	4	US-09-252-991A-16880	Sequence 16880, A
40	40	50.0	324	4	US-09-252-991A-16700	Sequence 16700, A
41	40	50.0	409	4	US-09-252-991A-28072	Sequence 28072, A
42	40	50.0	630	4	US-09-252-991A-26324	Sequence 26324, A
43	40	50.0	632	4	US-09-252-991A-24235	Sequence 24235, A
44	39.5	49.4	498	4	US-09-252-991A-20702	Sequence 20702, A
45	39.5	49.4	525	4	US-09-252-991A-23870	Sequence 23870, A

ALIGNMENTS

RESULT 1
US-09-621-976-6521
; Sequence 6521, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6521
; LENGTH: 71
; TYPE: PPT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 62
; OTHER INFORMATION: Xaa = Ala,Ser
; NAME/KEY: UNSURE
; LOCATION: 43
; OTHER INFORMATION: Xaa = Leu,Val
US-09-621-976-6521

Query Match 100.0% Score 80; DB 4; Length 71;
Best Local Similarity 100.0%; Pred. No. 9.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APRAVFSPSIVGRPRH 15
| | | | | | | | | | | | | | |
Db 26 APRAVFSPSIVGRPRH 40

RESULT 2
US-08-609-236-6
; Sequence 6, Application US/08609236
; Patent No. 6087398
; GENERAL INFORMATION:
; APPLICANT: Steven R. Goodman
; TITLE OF INVENTION: No. 6087398el Sickle Cell Anemia Treatment
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McGregor & Adler, LLP
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA

```

; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,236
; FILING DATE: March 1, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/002,288
; FILING DATE: August 14, 1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Benjamin Aaron Adler, Ph.D.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5807
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6908
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374
; TYPE: Amino acid
; STRANDEDNESS:
; TOPOLOGY: Linear
; MOLECULE TYPE: Protein
; DESCRIPTION: No
; HYPOTHETICAL: No
; ANTI-SENSE: No
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
US-08-609-236-6

Query Match 100.0%; Score 80; DB 3; Length 374;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRVFPSPISVGPRH 15
Db 25 APRVFPSPISVGPRH 39
|||||

RESULT 3
US-08-494-151-14
; Sequence 14, Application US/08494151
; Patent No. 5840528
; GENERAL INFORMATION:
; APPLICANT: Van Oyen, Albert Johannes Joseph
; TITLE OF INVENTION: Transformation of Pfaffia rhodozyma
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/494,151
; FILING DATE: 23-JUN-1995
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20039.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-494-151-14

Query Match 100.0%; Score 80; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRVFPSPISVGPRH 15
Db 26 APRVFPSPISVGPRH 40
|||||

RESULT 4
US-09-106-217-16
; Sequence 16, Application US/09106217
; Patent No. 6063576
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Olson, Timothy M.
; TITLE OF INVENTION: Actin Mutations in Dilated
; TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; STREET: Tower
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,217
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION: /
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 2323-125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-106-217-16

Query Match 100.0%; Score 80; DB 3; Length 375;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRVFPSPISVGPRH 15

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Db 26 APRVFPISVGRPRH 40

RESULT 5

US-09-171-337A-7

; Sequence 7, Application US/09171337A

; Patent No. 6300095

; GENERAL INFORMATION:

; APPLICANT: BARREDO FUENTE, Jose Luis

; RODRIGUEZ SAIZ, Marta

; COLLADOS DE LA VIEJA, Alfonso J.

; MORENO VALLE, Migueu Angel

; SALTO MALDONADO, Francisco

; DIEZ GARCIA, Bruno

; TITLE OF INVENTION: PROMOTERS OF THE GENES GLUTAMATE

; DESHYDROGENASE, -N-ACETYLHEXOSAMINIDASE

; AND -ACTIN AND THEIR USE IN FILAMENTOUS

; FUNGI EXPRESSION, SECRETION AND ANTISENSE

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LADAS & PARRY

; STREET: 26 WEST 61 STREET

; CITY: NEW YORK

; STATE: NY

; COUNTRY: USA

; ZIP: 10023

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3-1/4" Disk 1.44MB

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11

; SOFTWARE: WordPerfect 8 for Windows

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/171,337A

; FILING DATE: 14-May-1999

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/ES98/00056

; FILING DATE: 5-MAR-1998

; APPLICATION NUMBER: ES9700482

; FILING DATE: 5-MAR-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: MASS, Clifford J.

; REGISTRATION NUMBER: 30,086

; (C) REF./DOCKET NO.: U-011948-3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 233288

; INFORMATION FOR SEQ ID NO: 7

; SEQUENCE CHARACTERISTICS:

; LENGTH: 375 amino acids

; TYPE: amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; ORIGINAL SOURCE:

; ORGANISM: Penicillium chrysogenum

; FEATURE:

; OTHER INFORMATION: amino acid sequence of the -actin

; protein with a molecular weight of

; 41760 Da.

; SEQUENCE DESCRIPTION: SEQ ID NO: 7

US-09-171-337A-7

Query Match 100.0%; Score 80; DB 3; Length 375;

Best Local Similarity 100.0%; Pred. No. 5.7e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRVFPISVGRPRH 15

|||||

Db 26 APRVFPISVGRPRH 40

|||||

RESULT 6

US-09-171-337A-8

; Sequence 7, Application US/09631022

; Patent No. 6558921

; GENERAL INFORMATION:

; APPLICANT: BARREDO FUENTE, Jose Luis

; RODRIGUEZ SAIZ, Marta

; Sequence 8, Application US/09171337A

; Patent No. 6300095

; GENERAL INFORMATION:

; APPLICANT: BARREDO FUENTE, Jose Luis

; RODRIGUEZ SAIZ, Marta

; COLLADOS DE LA VIEJA, Alfonso J.

; MORENO VALLE, Migueu Angel

; SALTO MALDONADO, Francisco

; DIEZ GARCIA, Bruno

; TITLE OF INVENTION: PROMOTERS OF THE GENES GLUTAMATE

; DESHYDROGENASE, -N-ACETYLHEXOSAMINIDASE

; AND -ACTIN AND THEIR USE IN FILAMENTOUS

; FUNGI EXPRESSION, SECRETION AND ANTISENSE

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LADAS & PARRY

; STREET: 26 WEST 61 STREET

; CITY: NEW YORK

; STATE: NY

; COUNTRY: USA

; ZIP: 10023

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3-1/4" Disk 1.44MB

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11

; SOFTWARE: WordPerfect 8 for Windows

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/171,337A

; FILING DATE: 14-May-1999

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/ES98/00056

; FILING DATE: 5-MAR-1998

; APPLICATION NUMBER: ES9700482

; FILING DATE: 5-MAR-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: MASS, Clifford J.

; REGISTRATION NUMBER: 30,086

; (C) REF./DOCKET NO.: U-011948-3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 233288

; INFORMATION FOR SEQ ID NO: 8

; SEQUENCE CHARACTERISTICS:

; LENGTH: 375 amino acids

; TYPE: amino acids

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: Peptide

; ORIGINAL SOURCE:

; ORGANISM: Acremonium chrysogenum

; FEATURE:

; OTHER INFORMATION: amino acid sequence of the -actin

; protein with a molecular weight of

; 41612 Da.

; SEQUENCE DESCRIPTION: SEQ ID NO: 8

US-09-171-337A-8

Query Match 100.0%; Score 80; DB 3; Length 375;

Best Local Similarity 100.0%; Pred. No. 5.7e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRVFPISVGRPRH 15

|||||

Db 26 APRVFPISVGRPRH 40

|||||

RESULT 7

US-09-631-022-7

; Sequence 7, Application US/09631022

; Patent No. 6558921

; GENERAL INFORMATION:

; APPLICANT: BARREDO FUENTE, Jose Luis

; RODRIGUEZ SAIZ, Marta

COLLADOS DE LA VIEJA, Alfonso J.
MORENO VALLE Migueul Angel
SALTO MALDONADO, Francisco
DIEZ GARCIA, Bruno
TITLE OF INVENTION: PROMOTERS OF THE GENES GLUTAMATE
DESHYDROGENASE, -N-ACETYLHEXOSAMINIDASE
AND -ACTIN AND THEIR USE IN FILAMENTOUS
FUNGI EXPRESSION, SECRETION AND ANTISENSE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: LADAS & PARRY
STREET: 26 WEST 61 STREET
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10023
COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/4" Disk 1.44MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11
SOFTWARE: WordPerfect 8 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/631,022
FILING DATE: 02-Aug-2000
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/171,337
FILING DATE: 14-MAY-1999
APPLICATION NUMBER: PCT/ES98/00056
FILING DATE: 5-MAR-1998
APPLICATION NUMBER: ES9700482
FILING DATE: 5-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: MASS, Clifford J.
REGISTRATION NUMBER: 30,086
(C) REF./DOCKET NO.: U-02886-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 233288
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Penicillium chrysogenum
FEATURE:
OTHER INFORMATION: amino acid sequence of the -actin
protein with a molecular weight of
41760 Da.
SEQUENCE DESCRIPTION: SEQ ID NO: 7
US-09-631-022-7
Query Match 100.0%; Score 80; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APRAVFPSIVGRPRH 15
DB 26 APRAVFPSIVGRPRH 40
RESULT 8
US-09-631-022-8
Sequence 8, Application US/09631022
Patent No. 6558921
GENERAL INFORMATION:
APPLICANT: BARREDO FUENTE, Jose Luis
COLLADOS DE LA VIEJA, Alfonso J.
MORENO VALLE, Migueul Angel
SALTO MALDONADO, Francisco

DIEZ GARCIA, Bruno
TITLE OF INVENTION: PROMOTERS OF THE GENES GLUTAMATE
DESHYDROGENASE, -N-ACETYLHEXOSAMINIDASE
AND -ACTIN AND THEIR USE IN FILAMENTOUS
FUNGI EXPRESSION, SECRETION AND ANTISENSE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: LADAS & PARRY
STREET: 26 WEST 61 STREET
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10023
COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/4" Disk 1.44MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11
SOFTWARE: WordPerfect 8 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/631,022
FILING DATE: 02-Aug-2000
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/171,337
FILING DATE: 14-MAY-1999
APPLICATION NUMBER: PCT/ES98/00056
FILING DATE: 5-MAR-1998
APPLICATION NUMBER: ES9700482
FILING DATE: 5-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: MASS, Clifford J.
REGISTRATION NUMBER: 30,086
(C) REF./DOCKET NO.: U-02886-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 233288
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Acremonium chrysogenum
FEATURE:
OTHER INFORMATION: amino acid sequence of the -actin
protein with a molecular weight of
41612 Da.
SEQUENCE DESCRIPTION: SEQ ID NO: 8
US-09-631-022-8
Query Match 100.0%; Score 80; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APRAVFPSIVGRPRH 15
DB 26 APRAVFPSIVGRPRH 40
RESULT 9
US-09-976-594-731
Sequence 731, Application US/09976594
Patent No. 6673549
GENERAL INFORMATION:
APPLICANT: Furness, Michael
BUCHBINDER, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12


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; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 731
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1837317CD1
US-09-976-594-731

Query Match      100.0%; Score 80; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 APRVFPSPVIGRPRH 15
      |||||
Db      26 APRVFPSPVIGRPRH 40

RESULT 10
US-08-588-113-2
; Sequence 2, Application US/08588113
; Patent No. 5710003
; GENERAL INFORMATION:
; APPLICANT: McHugh, Kirk M.
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR DETERMINING
; TITLE OF INVENTION: MALIGNANCY OF SMOOTH MUSCLE TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5710003ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/588,113
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Ralph, Rebecca L.
; REGISTRATION NUMBER: 35,152
; REFERENCE/DOCKET NUMBER: TJU-1652
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 376 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-588-113-2

Query Match      100.0%; Score 80; DB 1; Length 376;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 APRVFPSPVIGRPRH 15
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Db      27 APRVFPSPVIGRPRH 41

RESULT 11
US-09-949-016-6100
; Sequence 6100, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6100
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6100

Query Match      100.0%; Score 80; DB 4; Length 376;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 APRVFPSPVIGRPRH 15
      |||||
Db      27 APRVFPSPVIGRPRH 41

RESULT 12
US-09-106-217-2
; Sequence 2, Application US/09106217
; Patent No. 6063576
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Olson, Timothy M.
; TITLE OF INVENTION: Actin Mutations in Dilated
; TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Earnat & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; STREET: Tower
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,217
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 2323-125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-106-217-2
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Query Match 100.0%; Score 80; DB 3; Length 377;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRVFPFSIVGRPRH 15
Db 28 APRVFPFSIVGRPRH 42

RESULT 13

US-09-919-172-33
; Sequence 33, Application US/09919172
; Patent No. 6673545

; GENERAL INFORMATION:

; APPLICANT: Paris, Mary

; APPLICANT: Turner, Christopher M.

; TITLE OF INVENTION: PROSTATE CANCER MARKERS

; FILE REFERENCE: PA-0036 US

; CURRENT APPLICATION NUMBER: US/09/919,172

; CURRENT FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/222,469

; PRIOR FILING DATE: 2000-07-28

; NUMBER OF SEQ ID NOS: 102

; SOFTWARE: PERL Program

; SEQ ID NO 33

; LENGTH: 377

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc.feature

; OTHER INFORMATION: Incyte ID No. 6673545 1709118CD1

US-09-919-172-33

Query Match 100.0%; Score 80; DB 4; Length 377;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRVFPFSIVGRPRH 15
Db 28 APRVFPFSIVGRPRH 42

RESULT 14

US-09-917-254-53

; Sequence 53, Application US/09917254

; Patent No. 6703204

; GENERAL INFORMATION:

; APPLICANT: Mutter, George

; APPLICANT: Baak, Jan

; TITLE OF INVENTION: Prognostic Classification of Breast Cancer

; FILE REFERENCE: B0801/7224(JRV)

; CURRENT APPLICATION NUMBER: US/09/917,254

; CURRENT FILING DATE: 2001-07-27

; PRIOR APPLICATION NUMBER: US 60/222,093

; PRIOR FILING DATE: 2000-07-28

; NUMBER OF SEQ ID NOS: 102

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 53

; LENGTH: 377

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-09-917-254-53

Query Match 100.0%; Score 80; DB 4; Length 377;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRVFPFSIVGRPRH 15
Db 28 APRVFPFSIVGRPRH 42

RESULT 15

US-09-949-016-7721
; Sequence 7721, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7721
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-7721

Query Match 100.0%; Score 80; DB 4; Length 386;
Best Local Similarity 100.0%; Pred. No. 5.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRVFPFSIVGRPRH 15
Db 37 APRVFPFSIVGRPRH 51

Search completed: April 8, 2005, 12:07:33
Job time : 17.5333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 10:53:18 ; Search time 42.6667 Seconds
(without alignments)
116.718 Million cell updates/sec

Title: US-09-423-351C-1
Perfect score: 80
Sequence: 1 APRAVFPISVGRPH 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 331997259 residues

Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubaa/PTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
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- 15: /cgn2_6/ptodata/1/pubaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubaa/US10E_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	80	100.0	105	US-10-264-049-3601	Sequence 3601, Ap
2	80	100.0	135	US-10-767-701-47318	Sequence 47318, A
3	80	100.0	136	US-10-424-599-280811	Sequence 280811,
4	80	100.0	142	US-10-424-599-184471	Sequence 184471,
5	80	100.0	197	US-10-424-599-280810	Sequence 280810,
6	80	100.0	201	US-10-264-049-4308	Sequence 4308, Ap
7	80	100.0	204	US-10-264-049-4148	Sequence 4148, Ap
8	80	100.0	208	US-10-424-599-282905	Sequence 282905,
9	80	100.0	219	US-10-002-631C-56	Sequence 56, Appl
10	80	100.0	230	US-10-767-701-42770	Sequence 42770, A
11	80	100.0	342	US-10-108-260A-4008	Sequence 4008, Ap
12	80	100.0	347	US-10-424-599-283333	Sequence 283333,
13	80	100.0	371	US-10-322-281-68	Sequence 68, Appl

14	80	100.0	375	14	US-10-205-194-93	Sequence 93, Appl
15	80	100.0	375	14	US-10-316-253-88	Sequence 88, Appl
16	80	100.0	375	15	US-10-369-493-1786	Sequence 1786, Ap
17	80	100.0	375	15	US-10-369-493-2436	Sequence 2436, Ap
18	80	100.0	375	15	US-10-369-493-5927	Sequence 5927, Ap
19	80	100.0	375	15	US-10-205-331-94	Sequence 94, Appl
20	80	100.0	375	15	US-10-260-708-82	Sequence 82, Appl
21	80	100.0	375	16	US-10-477-369-1	Sequence 1, Appl
22	80	100.0	376	15	US-10-341-434-101	Sequence 101, Appl
23	80	100.0	376	16	US-10-437-963-179917	Sequence 179917,
24	80	100.0	376	16	US-10-437-963-202420	Sequence 202420,
25	80	100.0	376	16	US-10-767-701-45677	Sequence 45677, A
26	80	100.0	376	16	US-10-767-701-46090	Sequence 46090, A
27	80	100.0	377	9	US-09-919-172-33	Sequence 33, Appl
28	80	100.0	377	14	US-10-338-777-52	Sequence 52, Appl
29	80	100.0	377	15	US-10-236-031B-64	Sequence 64, Appl
30	80	100.0	377	15	US-10-424-599-162009	Sequence 162009,
31	80	100.0	377	15	US-10-424-599-222816	Sequence 222816,
32	80	100.0	377	15	US-10-424-599-223492	Sequence 223492,
33	80	100.0	377	15	US-10-424-599-283336	Sequence 283336,
34	80	100.0	377	15	US-10-425-114-66124	Sequence 66124, A
35	80	100.0	377	16	US-10-333-680-4	Sequence 4, Appl
36	80	100.0	377	16	US-10-437-963-121952	Sequence 121952,
37	80	100.0	377	16	US-10-437-963-148877	Sequence 148877,
38	80	100.0	377	16	US-10-437-963-198295	Sequence 198295,
39	80	100.0	377	16	US-10-767-701-47239	Sequence 47239, A
40	80	100.0	378	15	US-10-425-114-36824	Sequence 36824, A
41	80	100.0	378	15	US-10-425-114-52458	Sequence 52458, A
42	80	100.0	378	15	US-10-425-114-59265	Sequence 59265, A
43	80	100.0	378	15	US-10-425-114-59967	Sequence 59967, A
44	80	100.0	378	15	US-10-425-114-61003	Sequence 61003, A
45	80	100.0	378	15	US-10-425-114-62783	Sequence 62783, A

ALIGNMENTS

RESULT 1
US-10-264-049-3601
; Sequence 3601, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133PI
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: Patent In Ver. 3.1
; SEQ ID NO 3601
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (103)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-3601

Query Match 100.0%; Score 80; DB 15; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRAVFPISVGRPH 15
DB 27 APRAVFPISVGRPH 41

RESULT 2

US-10-767-701-47318

; Sequence 47318, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 47318
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(135)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C105_2.pep
US-10-767-701-47318

Query Match 100.0%; Score 80; DB 16; Length 135;

Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRAVFPISIVGRPRH 15
Db 28 APRAVFPISIVGRPRH 42

RESULT 3

US-10-424-599-280811
; Sequence 280811, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 280811
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_95595C.1.pep
US-10-424-599-280811

Query Match 100.0%; Score 80; DB 15; Length 136;

Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRAVFPISIVGRPRH 15
Db 28 APRAVFPISIVGRPRH 42

RESULT 4

US-10-424-599-184471
; Sequence 184471, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 184471
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_137594C.1.pep
US-10-424-599-184471

Query Match 100.0%; Score 80; DB 15; Length 142;

Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRAVFPISIVGRPRH 15
Db 35 APRAVFPISIVGRPRH 49

RESULT 5

US-10-424-599-280810
; Sequence 280810, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 280810
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(197)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_95594C.1.pep
US-10-424-599-280810

Query Match 100.0%; Score 80; DB 15; Length 197;

Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRAVFPISIVGRPRH 15
Db 28 APRAVFPISIVGRPRH 42

RESULT 6

US-10-264-049-4308
; Sequence 4308, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PAL33P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07

; PRIOR APPLICATION NUMBER: US 60/209,467
 ; PRIOR FILING DATE: 2000-06-07
 ; NUMBER OF SEQ ID NOS: 4360
 ; SOFTWARE: PatentIn Ver. 3.1
 ; SEQ ID NO 4308
 ; LENGTH: 201
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (135)
 ; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (136)
 ; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (143)
 ; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (144)
 ; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (145)
 ; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (151)
 ; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (159)
 ; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (172)
 ; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (174)
 ; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (180)
 ; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
 ; FEATURE:
 ; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

Query Match 100.0%; Score 80; DB 15; Length 201;
 Best Local Similarity 100.0%; Pred. No. 3.3e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRAVPPSIVGRPRH 15
 DB 43 APRAVPPSIVGRPRH 57

RESULT 7
 US-10-264-049-4148
 ; Sequence 4148, Application US/10264049
 ; Publication No. US20040005579A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Birse et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PA133PI
 ; CURRENT APPLICATION NUMBER: US/10/264,049
 ; CURRENT FILING DATE: 2002-10-04

; PRIOR APPLICATION NUMBER: PCT/US01/18569
 ; PRIOR FILING DATE: 2001-06-07
 ; PRIOR APPLICATION NUMBER: US 60/209,467
 ; PRIOR FILING DATE: 2000-06-07
 ; NUMBER OF SEQ ID NOS: 4360
 ; SOFTWARE: PatentIn Ver. 3.1
 ; SEQ ID NO 4148
 ; LENGTH: 204
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-264-049-4148

Query Match 100.0%; Score 80; DB 15; Length 204;
 Best Local Similarity 100.0%; Pred. No. 3.3e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRAVPPSIVGRPRH 15
 DB 46 APRAVPPSIVGRPRH 60

RESULT 8
 US-10-424-599-282905
 ; Sequence 282905, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 282905
 ; LENGTH: 208
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(208)
 ; OTHER INFORMATION: unsure at all Xaa locations
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_97486C.1.pap
 ; US-10-424-599-282905

Query Match 100.0%; Score 80; DB 15; Length 208;
 Best Local Similarity 100.0%; Pred. No. 3.4e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRAVPPSIVGRPRH 15
 DB 28 APRAVPPSIVGRPRH 42

RESULT 9
 US-10-002-631C-56
 ; Sequence 56, Application US/10002631C
 ; Publication No. US20030157486A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Graff, Jonathon M.
 ; APPLICANT: Muenster, Matthew
 ; TITLE OF INVENTION: METHODS TO IDENTIFY SIGNAL SEQUENCES
 ; FILE REFERENCE: A34943 090495.0243
 ; CURRENT APPLICATION NUMBER: US/10/002,631C
 ; CURRENT FILING DATE: 2001-10-31
 ; PRIOR APPLICATION NUMBER: 60/300,309
 ; PRIOR FILING DATE: 2001-06-21
 ; NUMBER OF SEQ ID NOS: 324
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 56

```
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-631C-56

Query Match      100.0%; Score 80; DB 14; Length 219;
Best Local Similarity 100.0%; Pred. No. 3.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRAVFPISIVGRPRH 15
Db 53 APRAVFPISIVGRPRH 67
|||||

RESULT 10
US-10-767-701-42770
; Sequence 42770, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 42770
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C17410_1.pep
US-10-767-701-42770

Query Match      100.0%; Score 80; DB 16; Length 230;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRAVFPISIVGRPRH 15
Db 28 APRAVFPISIVGRPRH 42
|||||

RESULT 11
US-10-108-260A-4008
; Sequence 4008, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4008
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-4008

Query Match      100.0%; Score 80; DB 15; Length 342;
Best Local Similarity 100.0%; Pred. No. 5.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRAVFPISIVGRPRH 15
Db 28 APRAVFPISIVGRPRH 42
|||||

RESULT 12
US-10-108-260A-4008
; Sequence 4008, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4008
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-4008

Query Match      100.0%; Score 80; DB 15; Length 342;
Best Local Similarity 100.0%; Pred. No. 5.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRAVFPISIVGRPRH 15
Db 28 APRAVFPISIVGRPRH 42
|||||

RESULT 13
US-10-322-281-68
; Sequence 68, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-281-68

Query Match      100.0%; Score 80; DB 16; Length 371;
Best Local Similarity 100.0%; Pred. No. 6.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRAVFPISIVGRPRH 15
Db 26 APRAVFPISIVGRPRH 40
|||||

RESULT 14
US-10-205-194-93
; Sequence 93, Application US/10205194
; Publication No. US20030134301A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brookbank, Robert
; APPLICANT: Pinnoch, Robert
US-10-205-194-93

Query Match      100.0%; Score 80; DB 16; Length 371;
Best Local Similarity 100.0%; Pred. No. 6.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRAVFPISIVGRPRH 15
Db 26 APRAVFPISIVGRPRH 40
|||||

US-10-424-599-283333
; Sequence 283333, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 283333
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(347)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_97873C.1.pep
US-10-424-599-283333

Query Match      100.0%; Score 80; DB 15; Length 347;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRAVFPISIVGRPRH 15
Db 28 APRAVFPISIVGRPRH 42
|||||
```

```

; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018201
; CURRENT APPLICATION NUMBER: US/10/205,194
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Rattus rattus
; FEATURE:
; OTHER INFORMATION: Cytoplasmic gamma isoform of actin
US-10-205-194-93

```

```

Query Match      100.0%; Score 80; DB 14; Length 375;
Best Local Similarity 100.0%; Pred. No. 6.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 APRVFPISIVGRPRH 15
      |||||
DB      26 APRVFPISIVGRPRH 40

```

```

RESULT 15
US-10-316-253-88
; Sequence 88, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-88

```

```

Query Match      100.0%; Score 80; DB 14; Length 375;
Best Local Similarity 100.0%; Pred. No. 6.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 APRVFPISIVGRPRH 15
      |||||
DB      26 APRVFPISIVGRPRH 40

```

Search completed: April 8, 2005, 12:50:57
Job time : 43.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 9.33333 Seconds
(without alignments)
154.634 Million cell updates/sec

Title: US-09-423-351C-1

Perfect score: 80

Sequence: 1 APRAVFFSIVGRPRH 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	80	100.0	43	2 A43616	actin alpha, cardi
2	80	100.0	86	2 C43616	actin beta, cyto
3	80	100.0	137	2 A28258	actin 5C - fruit f
4	80	100.0	140	2 S03109	actin - pin mould
5	80	100.0	158	2 I49465	alpha-cardiac acti
6	80	100.0	195	2 S20097	actin 85C - potato
7	80	100.0	213	2 A61043	actin CAL5 - sea g
8	80	100.0	308	2 A03000	actin 3 - fruit fl
9	80	100.0	328	2 S05430	actin beta - grass
10	80	100.0	336	2 T04085	actin - maize (fra
11	80	100.0	362	2 A26559	actin type 5, cyto
12	80	100.0	370	2 A29664	actin - sea urchin
13	80	100.0	374	1 ATEOB	actin beta - bovin
14	80	100.0	374	1 ATEOB	actin gamma - bovi
15	80	100.0	374	2 JC5818	gamma-actin - huma
16	80	100.0	375	1 ATEBOM	actin, aortic smoo
17	80	100.0	375	1 ATRB	actin, skeletal mu
18	80	100.0	375	1 ATRTC	actin beta - rat
19	80	100.0	375	1 A48324	actin beta, cytosk
20	80	100.0	375	1 ATRAX	actin - Acanthamo
21	80	100.0	375	1 ATRB	actin - yeast (Sac
22	80	100.0	375	1 ATCHB	actin beta - chick
23	80	100.0	375	1 ATDO	actin - slime mold
24	80	100.0	375	1 ATHUB	actin beta - human
25	80	100.0	375	1 ATHUG	actin gamma 1 - hu
26	80	100.0	375	1 ATMSB	actin beta - mouse
27	80	100.0	375	1 ATMSG	actin gamma - mous
28	80	100.0	375	1 ATRBB	actin beta, non-mu
29	80	100.0	375	1 ATZM1	actin - maize

actin - yeast (Sac
actin gamma, cytos
actin, cytosolic (
actin gamma - Emer
actin 1 - Pneumocy
hypothetical prote
actin - yeast (Klu
actin - fission ye
actin beta-2, cyto
actin beta-1, cyto
actin beta, cytos
actin beta - goose
actin alpha, cardi
actin - imperfect
actin - Phaffia rh
actin 7 - fruit fl

ALIGNMENTS

RESULT 1

A43616

actin alpha, cardiac - chicken (fragment)

C:Species: Gallus gallus (chicken)

C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 16-Jul-1999

C:Accession: A43616

R:Paterson, B.M.; Eldridge, J.D.

Science 224, 1436-1438, 1984

A:Title: alpha-Cardiac actin is the major sarcomeric isoform expressed in embryonic avia

A:Reference number: A43616; MUID:84223949; PMID:6729461

A:Accession: A43616

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-43 <PAT>

A:Cross-references: GB:M10607

C:Superfamily: actin

C:Keywords: cardiac muscle; heart

Query Match 100.0%; Score 80; DB 2; Length 43;

Best Local Similarity 100.0%; Pred. No. 6.2e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APRAVFFSIVGRPRH 15

|||||

Db 28 APRAVFFSIVGRPRH 42

RESULT 2

C43616

actin beta, cytosolic - chicken (fragment)

C:Species: Gallus gallus (chicken)

C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004

C:Accession: C43616

R:Paterson, B.M.; Eldridge, J.D.

Science 224, 1436-1438, 1984

A:Title: alpha-Cardiac actin is the major sarcomeric isoform expressed in embryonic avia

A:Reference number: A43616; MUID:84223949; PMID:6729461

A:Accession: C43616

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-86 <PAT>

A:Cross-references: UNIPROT:Q90736; GB:K02173; NID:g211054; PIDN:AAA98513.1; PID:g211055

C:Superfamily: actin

F:73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 80; DB 2; Length 86;

Best Local Similarity 100.0%; Pred. No. 1.3e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APRAVFFSIVGRPRH 15

|||||

Db 26 APRVFPFSIVGRPRH 40

RESULT 3

A28258

actin 5C - fruit fly (*Drosophila melanogaster*)

C:Species: *Drosophila melanogaster*

C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004

C:Accession: A28258

R:Vigoreaux, J.O.; Tobin, S.L.

Genes Dev. 1, 1161-1171, 1987

A:Title: Stage-specific selection of alternative transcriptional initiation sites from

A:Reference number: A28258; MUID:88112795; PMID:3123314

A:Accession: A28258

A:Molecule type: mRNA

A:Residues: 1-137 <VIG>

A:CROSS-references: UNIPROT:P10987

A:Note: the authors translated the codon GAG for residue 96 as Gly

C:Genetics:

A:Gene: FlyBase:Act5C

A:CROSS-references: FlyBase:FBgn0000042

C:Superfamily: actin

C:Keywords: methylated amino acid

F,74/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 80; DB 2; Length 137;

Best Local Similarity 100.0%; Pred. No. 2.1e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRVFPFSIVGRPRH 15

Db 27 APRVFPFSIVGRPRH 41

RESULT 4

S03109

actin - pin mould (*Absidia glauca*) (fragment)

C:Species: *Absidia glauca*

C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

C:Accession: S03109

R:Burmester, A.; Weigel, C.; Woestener, J.

submitted to the EMBL Data Library, June 1988

A:Reference number: S03109

A:Accession: S03109

A:Molecule type: DNA

A:Residues: 1-140 <BUR>

A:CROSS-references: UNIPROT:P10982; EMBL:X07999; NID:G2303; PIDN:CAA30804.1; PID:g578097

C:Genetics:

A:Gene: act1

A:Introns: 9/3; 31/3

C:Superfamily: actin

C:Keywords: methylated amino acid

F,75/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 80; DB 2; Length 140;

Best Local Similarity 100.0%; Pred. No. 2.1e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRVFPFSIVGRPRH 15

Db 28 APRVFPFSIVGRPRH 42

RESULT 5

I49465

alpha-cardiac actin - mouse (fragment)

C:Species: *Mus musculus* (house mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I49465; I49466

R:Garner, I.; Minty, A.J.; Alonso, S.; Barton, P.J.R.; Buckingham, M.E.

EMBO J. 5, 2559-2567, 1986

A:Title: A 5' duplication of the alpha-cardiac actin gene in BALB/c mice is associated

A:Reference number: I49465; MUID:87053822; PMID:3023046

Db 26 APRVFPFSIVGRPRH 40

RESULT 3

A28258

actin 5C - fruit fly (*Drosophila melanogaster*)

C:Species: *Drosophila melanogaster*

C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004

C:Accession: A28258

R:Vigoreaux, J.O.; Tobin, S.L.

Genes Dev. 1, 1161-1171, 1987

A:Title: Stage-specific selection of alternative transcriptional initiation sites from

A:Reference number: A28258; MUID:88112795; PMID:3123314

A:Accession: A28258

A:Molecule type: mRNA

A:Residues: 1-137 <VIG>

A:CROSS-references: UNIPROT:P10987

A:Note: the authors translated the codon GAG for residue 96 as Gly

C:Genetics:

A:Gene: FlyBase:Act5C

A:CROSS-references: FlyBase:FBgn0000042

C:Superfamily: actin

C:Keywords: methylated amino acid

F,74/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 80; DB 2; Length 137;

Best Local Similarity 100.0%; Pred. No. 2.1e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRVFPFSIVGRPRH 15

Db 27 APRVFPFSIVGRPRH 41

RESULT 4

S03109

actin - pin mould (*Absidia glauca*) (fragment)

C:Species: *Absidia glauca*

C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

C:Accession: S03109

R:Burmester, A.; Weigel, C.; Woestener, J.

submitted to the EMBL Data Library, June 1988

A:Reference number: S03109

A:Accession: S03109

A:Molecule type: DNA

A:Residues: 1-140 <BUR>

A:CROSS-references: UNIPROT:P10982; EMBL:X07999; NID:G2303; PIDN:CAA30804.1; PID:g578097

C:Genetics:

A:Gene: act1

A:Introns: 9/3; 31/3

C:Superfamily: actin

C:Keywords: methylated amino acid

F,75/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 80; DB 2; Length 140;

Best Local Similarity 100.0%; Pred. No. 2.1e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRVFPFSIVGRPRH 15

Db 28 APRVFPFSIVGRPRH 42

RESULT 5

I49465

alpha-cardiac actin - mouse (fragment)

C:Species: *Mus musculus* (house mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I49465; I49466

R:Garner, I.; Minty, A.J.; Alonso, S.; Barton, P.J.R.; Buckingham, M.E.

EMBO J. 5, 2559-2567, 1986

A:Title: A 5' duplication of the alpha-cardiac actin gene in BALB/c mice is associated

A:Reference number: I49465; MUID:87053822; PMID:3023046

A:Accession: I49465

A>Status: translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-158 <RES>

A:CROSS-references: UNIPROT:Q61273; GB:M26775; NID:G191646; PIDN:AAA37165.1; PID:g553858

A:Accession: I49466

A:Molecule type: DNA

A:Residues: 8-158 <RE2>

A:CROSS-references: GB:M26776; NID:G191649; PIDN:AAA37166.1; PID:g553859

A:Experimental source: adult cardiac muscle, BALB/c mice

C:Genetics:

A:Introns: 50/3

C:Superfamily: actin

C:Keywords: cardiac muscle; heart

Query Match 100.0%; Score 80; DB 2; Length 158;

Best Local Similarity 100.0%; Pred. No. 2.4e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRVFPFSIVGRPRH 15

Db 35 APRVFPFSIVGRPRH 49

RESULT 6

S20097

actin 85c - potato (fragment)

C:Species: *Solanum tuberosum* (potato)

C>Date: 22-Nov-1993 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004

C:Accession: S20097

R:Drouin, G.; Dover, G.A.

J. Mol. Evol. 31, 132-150, 1990

A:Title: Independent gene evolution in the potato actin gene family demonstrated by phyl

A:Reference number: S20092; MUID:91012599; PMID:2120451

A:Accession: S20097

A:Molecule type: DNA

A:Residues: 1-195 <DRO>

A:CROSS-references: UNIPROT:P30170; EMBL:X55747; NID:G21541; PIDN:CAA39277.1; PID:G13455

C:Genetics:

A:Introns: 132/1

C:Superfamily: actin

C:Keywords: cytoskeleton; structural protein

Query Match 100.0%; Score 80; DB 2; Length 195;

Best Local Similarity 100.0%; Pred. No. 3e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRVFPFSIVGRPRH 15

Db 8 APRVFPFSIVGRPRH 22

RESULT 7

A61043

actin CA15 - sea squirt (*Styela clava*) (fragments)

C:Species: *Styela clava*

C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C:Accession: A61043

R:Beach, R.L.; Jeffery, W.R.

Dev. Genet. 11, 2-14, 1990

A:Title: Temporal and spatial expression of a cytoskeletal actin gene in the ascidian St

A:Reference number: A61043; MUID:90298580; PMID:2361333

A:Accession: A61043

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-213 <BEA>

A:CROSS-references: UNIPROT:Q7M3Y7

C:Comment: This sequence is expressed in cells undergoing rapid cell division.

C:Superfamily: actin

C:Keywords: cytoskeleton; methylated amino acid; mitosis; structural protein

F,73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 80; DB 2; Length 213;
 Best Local Similarity 100.0%; Pred. No. 3.3e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRAVFPSIVGRPRH 15
 DB 26 APRAVFPSIVGRPRH 40
 |||||
 |||||

RESULT 8
 A03000
 actin 3 - fruit fly (*Drosophila melanogaster*) (fragments)
 C:Species: *Drosophila melanogaster*
 C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
 C:Accession: A03000
 R:Fyrberg, E.A.; Bond, B.J.; Hershey, N.D.; Mixter, K.S.; Davidson, N.
 Cell 24, 107-116, 1981
 A>Title: The actin genes of *Drosophila*: protein coding regions are highly conserved but
 A:Reference number: A03000; MUID:81210174; PMID:6263481
 A:Accession: A03000
 A:Molecule type: DNA
 A:Residues: 1-308 <FYR>
 A:CROSS-references: UNIPROT:P02572
 A>Note: there are 68 unsequenced residues between positions 160 and 161. Partial sequen
 C:Genetics:
 A:Gene: FlyBase:Act42A
 A:CROSS-references: FlyBase:FBgn0000043
 A:Map position: 42A
 C:Superfamily: actin
 C:Keywords: methylated amino acid
 F:74/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 80; DB 2; Length 308;
 Best Local Similarity 100.0%; Pred. No. 4.8e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRAVFPSIVGRPRH 15
 DB 27 APRAVFPSIVGRPRH 41
 |||||
 |||||

RESULT 9
 S05430
 actin beta - grass carp
 C:Species: *Ctenopharyngodon idella* (grass carp)
 C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
 C:Accession: S05430
 R:Liu, Z.; Zhu, Z.; Roberg, K.; Faras, A.J.; Guise, K.S.; Kapuscinski, A.R.; Hackett, P.
 Nucleic Acids Res. 17, 5850, 1989
 A>Title: The beta-actin gene of carp (*Ctenopharyngodon idella*).
 A:Reference number: S05430; MUID:89345185; PMID:2762162
 A:Accession: S05430
 A>Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-328 <LIU>
 A:CROSS-references: UNIPROT:P83751; EMBL:M25013
 C:Genetics:
 A:introns: 41/3; 121/3; 268/1
 C:Superfamily: actin
 C:Keywords: cytoskeleton; methylated amino acid
 F:73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 80; DB 2; Length 328;
 Best Local Similarity 100.0%; Pred. No. 5.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRAVFPSIVGRPRH 15
 DB 26 APRAVFPSIVGRPRH 40
 |||||
 |||||

RESULT 10

T04085
 actin - maize (fragment)
 C:Species: *Zea mays* (maize)
 C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C:Accession: T04085
 R:de Sa, M.; Drouin, G.
 Mol. Biol. Evol. 13, 1198-1212, 1996
 A>Title: Phylogeny and substitution rates of angiosperm actin genes.
 A:Reference number: Z15197; MUID:97051711; PMID:8896372
 A:Accession: T04085
 A>Status: preliminary; translated from GB/EMBL/DDBB
 A:Molecule type: DNA
 A:Residues: 1-336 <DES>
 A:CROSS-references: UNIPROT:P93638; EMBL:U60513; NID:g1498392; PIDN:AAB40107.1; PID:g1449
 C:Genetics:
 A:Gene: Maz63
 A>Note: Intron positions not resolved (incomplete sequence)
 C:Superfamily: actin
 C:Keywords: cytoskeleton; structural protein

Query Match 100.0%; Score 80; DB 2; Length 336;
 Best Local Similarity 100.0%; Pred. No. 5.3e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRAVFPSIVGRPRH 15
 DB 8 APRAVFPSIVGRPRH 22
 |||||
 |||||

RESULT 11
 A26559
 actin type 5, cytosolic - chicken
 C:Species: *Gallus gallus* (chicken)
 C>Date: 09-Sep-1987 #sequence_revision 09-Sep-1987 #text_change 05-Dec-1997
 C:Accession: A26559
 R:Bergsma, D.J.; Chang, K.S.; Schwartz, R.J.
 Mol. Cell. Biol. 5, 1151-1162, 1985
 A:Reference number: A26559; MUID:85213487; PMID:4000121
 A:Accession: A26559
 A:Molecule type: DNA
 A:Residues: 1-362 <BER>
 C:Superfamily: actin
 C:Keywords: cytosol; methylated amino acid
 F:74/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 80; DB 2; Length 362;
 Best Local Similarity 100.0%; Pred. No. 5.7e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRAVFPSIVGRPRH 15
 DB 27 APRAVFPSIVGRPRH 41
 |||||
 |||||

RESULT 12
 A29664
 actin - sea urchin (*Strongylocentrotus purpuratus*)
 C:Species: *Strongylocentrotus purpuratus* (purple urchin)
 C>Date: 15-Dec-1988 #sequence_revision 30-Sep-1991 #text_change 05-Dec-1997
 C:Accession: A29664
 R:Crain Jr., W.R.; Boshart, M.F.; Cooper, A.D.; Durica, D.S.; Nagy, A.; Steffen, D.
 J. Mol. Evol. 25, 37-45, 1987
 A>Title: The sequence of a sea urchin muscle actin gene suggests a gene conversion with
 A:Reference number: A29664; MUID:87311761; PMID:3114500
 A:Accession: A29664
 A:Molecule type: DNA
 A:Residues: 1-370 <CRA>
 A:CROSS-references: GB:X05739; GB:X05740; GB:X05741; GB:X05742; GB:X05743
 A>Note: the authors translated the codon CAG for residue 260 as Glu
 C:Superfamily: actin
 C:Keywords: methylated amino acid
 F:73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 80; DB 2; Length 370;
 Best Local Similarity 100.0%; Pred. No. 5.9e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APRAVFPSIVGRPRH 15
 |||||
 Db 26 APRAVFPSIVGRPRH 40
 |||||

RESULT 13

ATBOG

actin beta - bovine (tentative sequence)
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
 C:Accession: E14185; A39105; A02999; A14185
 R:Vandekerckhove, J.; Weber, K.
 Eur. J. Biochem. 90, 451-462, 1978
 A:Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain
 A:Reference number: A14185; MUID:79045349; PMID:213279
 A:Accession: E14185
 A:Molecule type: protein
 A:Residues: 1-374 <VAN>
 A:CROSS-references: UNIPROT:P60712
 A:Note: only peptides that differed in composition from the corresponding peptides of ra
 R:Degeen, J.L.; Neubauer, M.G.; Degen, S.J.F.; Seyfried, C.E.; Morris, D.R.
 J. Biol. Chem. 258, 12153-12162, 1983
 A:Title: Regulation of protein synthesis in mitogen-activated bovine lymphocytes. Analys
 A:Reference number: A39105; MUID:84032385; PMID:6195151
 A:Accession: A39105
 A:Molecule type: mRNA
 A:Residues: 76-227;344-374 <DEG>
 A:CROSS-references: GB:K00622; GB:K00623
 A:Note: actins beta and gamma were not distinguished in this study
 C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
 C:Superfamily: actin
 C:Keywords: blocked amino end; cell motility; cytoskeleton; methylated amino acid; micro
 F:1/Modified site: blocked amino end (Asp) (probably acetylated) #status experimental
 F:72/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 80; DB 1; Length 374;
 Best Local Similarity 100.0%; Pred. No. 5.9e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APRAVFPSIVGRPRH 15
 |||||
 Db 25 APRAVFPSIVGRPRH 39
 |||||

RESULT 14

ATBOG

actin gamma - bovine (tentative sequence)
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
 C:Accession: B14185; A02999
 R:Vandekerckhove, J.; Weber, K.
 Eur. J. Biochem. 90, 451-462, 1978
 A:Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain
 A:Reference number: A14185; MUID:79045349; PMID:213279
 A:Accession: B14185
 A:Molecule type: protein
 A:Residues: 1-374 <VAN>
 A:CROSS-references: UNIPROT:P02571
 A:Note: only peptides that differed in composition from the corresponding peptides of ra
 C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
 C:Superfamily: actin
 C:Keywords: blocked amino end; cell motility; cytoskeleton; methylated amino acid; micro
 F:1/Modified site: blocked amino end (Glu) (probably acetylated) #status experimental
 F:72/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 80; DB 1; Length 374;
 Best Local Similarity 100.0%; Pred. No. 5.9e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APRAVFPSIVGRPRH 15
 |||||
 Db 25 APRAVFPSIVGRPRH 39
 |||||

RESULT 15

JC5818

gamma-actin - human
 C:Species: Homo sapiens (man)
 C>Date: 20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
 C:Accession: JC5818; PC4501
 R:Hauschildt, S.; Schwarz, C.; Heine, H.; Ulmer, A.J.; Flad, H.D.; Rietschel, E.T.; Jens
 Biochem. Biophys. Res. Commun. 241, 670-674, 1997
 A:Title: Actin: A target of lipopolysaccharid-induced phosphorylation in human monocytes
 A:Reference number: JC5818; MUID:98096379; PMID:9434766
 A:Accession: JC5818
 A:Molecule type: protein
 A:Residues: 1-374 <HAU>
 A:CROSS-references: UNIPROT:P02571
 A:Experimental source: monocyte
 A:Accession: PC4501
 A:Molecule type: protein
 A:Residues: 1-61;84-112;147-190;196-209;215-253;335-358 <HA2>
 A:Experimental source: monocyte
 C:Comment: This protein is involved in a signal transduction that eventually leads to mo
 C:Superfamily: actin

Query Match 100.0%; Score 80; DB 2; Length 374;
 Best Local Similarity 100.0%; Pred. No. 5.9e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APRAVFPSIVGRPRH 15
 |||||
 Db 25 APRAVFPSIVGRPRH 39
 |||||

Search completed: April 8, 2005, 10:53:04
 Job time : 10.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 57.8667 Seconds
(without alignments)
132.739 Million cell updates/sec

Title: US-09-423-351C-1
Perfect score: 80
Sequence: 1 APRAVFPSIVGRPRH 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	80	100.0	20	2	Q8X127 magnaporthe
2	80	100.0	20	2	Q8X128 magnaporthe
3	80	100.0	20	2	Q96VW9 magnaporthe
4	80	100.0	20	2	Q96VW0 magnaporthe
5	80	100.0	20	2	Q96VW1 magnaporthe
6	80	100.0	20	2	Q96VW2 magnaporthe
7	80	100.0	20	2	Q9C2Z3 sclerotinia
8	80	100.0	20	2	Q9C2Z4 sclerotinia
9	80	100.0	20	2	Q9C2Z5 sclerotinia
10	80	100.0	20	2	Q9C2Z6 sclerotinia
11	80	100.0	20	2	Q9C2Z7 sclerotinia
12	80	100.0	20	2	Q9C2Z8 sclerotinia
13	80	100.0	20	2	Q9C2Z9 sclerotinia
14	80	100.0	20	2	Q9C300 sclerotinia
15	80	100.0	20	2	Q9C301 sclerotinia
16	80	100.0	20	2	Q9C302 sclerotinia
17	80	100.0	20	2	Q9C303 sclerotinia
18	80	100.0	20	2	Q9C304 sclerotinia
19	80	100.0	20	2	Q9C305 sclerotinia
20	80	100.0	20	2	Q9C306 sclerotinia
21	80	100.0	20	2	Q9C307 sclerotinia
22	80	100.0	20	2	Q9C308 sclerotinia
23	80	100.0	20	2	Q9C309 sclerotinia
24	80	100.0	20	2	Q9C310 sclerotinia
25	80	100.0	20	2	Q9C311 sclerotinia
26	80	100.0	20	2	Q9C312 sclerotinia
27	80	100.0	20	2	Q9C313 sclerotinia
28	80	100.0	20	2	Q9C314 sclerotinia
29	80	100.0	20	2	Q9C315 sclerotinia
30	80	100.0	20	2	Q9C316 sclerotinia
31	80	100.0	20	2	Q9C317 sclerotinia

32	80	100.0	20	2	Q9C318 sclerotinia
33	80	100.0	20	2	Q9C319 sclerotinia
34	80	100.0	20	2	Q9C320 sclerotinia
35	80	100.0	20	2	Q9C321 sclerotinia
36	80	100.0	20	2	Q9C322 sclerotinia
37	80	100.0	20	2	Q9C323 sclerotinia
38	80	100.0	20	2	Q9C324 sclerotinia
39	80	100.0	20	2	Q9C325 sclerotinia
40	80	100.0	20	2	Q9C326 sclerotinia
41	80	100.0	20	2	Q9C327 sclerotinia
42	80	100.0	20	2	Q9C328 sclerotinia
43	80	100.0	20	2	Q9C329 sclerotinia
44	80	100.0	20	2	Q9C330 sclerotinia
45	80	100.0	20	2	Q9C331 sclerotinia

ALIGNMENTS

RESULT 1
Q8X127 PRELIMINARY; PRT; 20 AA.
AC Q8X127;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Actin (Fragment).
OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthes.
OX NCBI_TaxID=148305;
RN [1]
RP SEQUENCE FROM N.A.
RA Couch B.C., Kohn L.M.;
RT "A multilocus gene genealogy concordant with host preference indicates segregation of a new species, Magnaporthes oryzae, from M. grisea.";
RL Mycologia 94:683-693 (2002).
DR EMBL; AY063735; AAL59410.1;
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 1
FT SEQUENCE 20 AA; 2141 MW; B06CCB097FA4BD CRC64;

Query Match 100.0%; Score 80; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRAVFPSIVGRPRH 15
Db 4 APRAVFPSIVGRPRH 18
|||||

RESULT 2
Q8X128 PRELIMINARY; PRT; 20 AA.
AC Q8X128;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Actin (Fragment).
OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthes.
OX NCBI_TaxID=148305;
RN [1]
RP SEQUENCE FROM N.A.
RA Couch B.C., Kohn L.M.;
RT "A multilocus gene genealogy concordant with host preference indicates segregation of a new species, Magnaporthes oryzae, from M. grisea.";
RL Mycologia 94:683-693 (2002).
DR EMBL; AY063734; AAL59409.1; -.

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DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 1 20
SQ SEQUENCE 20 AA; 2141 MW; B06CCBB097FA4ABD CRC64;

Query Match 100.0%; Score 80; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APRAVFPSIVGRPRH 15
Db 4 APRAVFPSIVGRPRH 18

RESULT 3
Q96VW9
ID Q96VW9 PRELIMINARY; PRT; 20 AA.
AC Q96VW9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Actin (Fragment).
GN Name=act;
OS Magnaporthe salvinii.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
OX NCBI_TaxID=165778;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS-1;
RA Couch B.C.; Kohn L.M.;
RT "A multilocus gene genealogy concordant with host preference indicates
RT segregation of a new species, Magnaporthe oryzae, from M. grisea.";
RL Mycologia 94:683-693(2002).
DR EMBL; AF395975; AAK77897.1; -.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 1 20
SQ SEQUENCE 20 AA; 2141 MW; B06CCBB097FA4ABD CRC64;

Query Match 100.0%; Score 80; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APRAVFPSIVGRPRH 15
Db 4 APRAVFPSIVGRPRH 18

RESULT 4
Q96VW0
ID Q96VW0 PRELIMINARY; PRT; 20 AA.
AC Q96VW0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Actin (Fragment).
GN Name=act;
OS Magnaporthe rhizophila.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
OX NCBI_TaxID=165777;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 96043;
RA Couch B.C.; Kohn L.M.;
RT "A multilocus gene genealogy concordant with host preference indicates
RT segregation of a new species, Magnaporthe oryzae, from M. grisea.";
```

```
RL Mycologia 94:683-693(2002).
DR EMBL; AF395974; AAK77896.1; -.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 1 20
SQ SEQUENCE 20 AA; 2141 MW; B06CCBB097FA4ABD CRC64;

Query Match 100.0%; Score 80; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APRAVFPSIVGRPRH 15
Db 4 APRAVFPSIVGRPRH 18

RESULT 5
Q96VW1
ID Q96VW1 PRELIMINARY; PRT; 20 AA.
AC Q96VW1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Actin (Fragment).
GN Name=act;
OS Magnaporthe poae (Kentucky bluegrass fungus).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
OX NCBI_TaxID=148304;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 6411;
RA Couch B.C.; Kohn L.M.;
RT "A multilocus gene genealogy concordant with host preference indicates
RT segregation of a new species, Magnaporthe oryzae, from M. grisea.";
RL Mycologia 94:683-693(2002).
DR EMBL; AF395973; AAK77895.1; -.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 1 20
SQ SEQUENCE 20 AA; 2141 MW; B06CCBB097FA4ABD CRC64;

Query Match 100.0%; Score 80; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APRAVFPSIVGRPRH 15
Db 4 APRAVFPSIVGRPRH 18

RESULT 6
Q96VW2
ID Q96VW2 PRELIMINARY; PRT; 20 AA.
AC Q96VW2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Actin (Fragment).
GN Name=act;
OS Magnaporthe rhizophila.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
OX NCBI_TaxID=165777;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 58114;
```

```
RA Couch B.C., Kohn L.M.;
RT "A multilocus gene genealogy concordant with host preference indicates
RT segregation of a new species, Magnaporthe oryzae, from M. grisea.";
RL Mycologia 94:683-693(2002).
DR EMBL; AF395972; AAK77894.1; -.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2141 MW; B06CCBB097FA4ABD CRC64;

Query Match 100.0%; Score 80; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRVFPSPVIGRPRH 15
DB 4 APRVFPSPVIGRPRH 18

RESULT 7
Q9C223 PRELIMINARY; PRT; 20 AA.
AC Q9C223;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Actin (Fragment).
GN Name=act;
OS Sclerotinia sclerotiorum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomyces;
OC Helotiales; Sclerotiniaceae; Sclerotinia.
OX NCBI_TaxID=5180;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W3-A3-5;
RX MEDLINE=21247026; PubMed=11348503;
RA Carbone I., Kohn L.M.;
RT "A microbial population-species interface: nested cladistic and
RT coalescent inference with multilocus data.";
RL Mol. Ecol. 10:947-964(2001).
DR EMBL; AF340964; AAK09783.1; -.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2141 MW; B06CCBB097FA4ABD CRC64;

Query Match 100.0%; Score 80; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRVFPSPVIGRPRH 15
DB 4 APRVFPSPVIGRPRH 18

RESULT 8
Q9C224 PRELIMINARY; PRT; 20 AA.
AC Q9C224;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Actin (Fragment).
GN Name=act;
OS Sclerotinia sclerotiorum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomyces;
OC Helotiales; Sclerotiniaceae; Sclerotinia.
OX NCBI_TaxID=5180;
```

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RN SEQUENCE FROM N.A.
RP STRAIN=W3-A3-2;
RX MEDLINE=21247026; PubMed=11348503;
RA Carbone I., Kohn L.M.;
RT "A microbial population-species interface: nested cladistic and
RT coalescent inference with multilocus data.";
RL Mol. Ecol. 10:947-964(2001).
DR EMBL; AF340963; AAK09782.1; -.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2141 MW; B06CCBB097FA4ABD CRC64;

Query Match 100.0%; Score 80; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRVFPSPVIGRPRH 15
DB 4 APRVFPSPVIGRPRH 18

RESULT 9
Q9C225 PRELIMINARY; PRT; 20 AA.
AC Q9C225;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Actin (Fragment).
GN Name=act;
OS Sclerotinia sclerotiorum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomyces;
OC Helotiales; Sclerotiniaceae; Sclerotinia.
OX NCBI_TaxID=5180;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W3-A1-5;
RX MEDLINE=21247026; PubMed=11348503;
RA Carbone I., Kohn L.M.;
RT "A microbial population-species interface: nested cladistic and
RT coalescent inference with multilocus data.";
RL Mol. Ecol. 10:947-964(2001).
DR EMBL; AF340962; AAK09781.1; -.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2141 MW; B06CCBB097FA4ABD CRC64;

Query Match 100.0%; Score 80; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRVFPSPVIGRPRH 15
DB 4 APRVFPSPVIGRPRH 18

RESULT 10
Q9C226 PRELIMINARY; PRT; 20 AA.
AC Q9C226;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Actin (Fragment).
GN Name=act;
OS Sclerotinia sclerotiorum.
```

```

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomyces;
OC Helotiales; Sclerotiniaceae; Sclerotinia.
OX NCBI_TaxID=5180;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W3-A1-3;
RX MEDLINE=21247026; PubMed=11348503;
RA Carbone I., Kohn L.M.;
RT "A microbial population-species interface: nested cladistic and
RT coalescent inference with multilocus data.";
RL Mol. Ecol. 10:947-964(2001).
DR EMBL; AF340961; AAK09780.1; -.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; F:structural constituent of cytoskeleton; IEA.
DR Pfam; PF00022; Actin; 1.
FT NON TER 1
SQ SEQUENCE 20 AA; 2141 MW; B06CCBB097FA4ABD CRC64;

Query Match 100.0%; Score 80; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRAVFPSIVGRPRH 15
DB 4 APRAVFPSIVGRPRH 18

RESULT 11
Q9C227
ID Q9C227 PRELIMINARY; PRT; 20 AA.
AC Q9C227;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Actin (Fragment).
GN Name=act;
OS Sclerotinia sclerotiorum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomyces;
OC Helotiales; Sclerotiniaceae; Sclerotinia.
OX NCBI_TaxID=5180;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W2-A4-5;
RX MEDLINE=21247026; PubMed=11348503;
RA Carbone I., Kohn L.M.;
RT "A microbial population-species interface: nested cladistic and
RT coalescent inference with multilocus data.";
RL Mol. Ecol. 10:947-964(2001).
DR EMBL; AF340960; AAK09779.1; -.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; F:structural constituent of cytoskeleton; IEA.
DR Pfam; PF00022; Actin; 1.
FT NON TER 1
SQ SEQUENCE 20 AA; 2141 MW; B06CCBB097FA4ABD CRC64;

Query Match 100.0%; Score 80; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRAVFPSIVGRPRH 15
DB 4 APRAVFPSIVGRPRH 18

RESULT 12
Q9C228
ID Q9C228 PRELIMINARY; PRT; 20 AA.
AC Q9C228;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

```

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DE Actin (Fragment).
GN Name=act;
OS Sclerotinia sclerotiorum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomyces;
OC Helotiales; Sclerotiniaceae; Sclerotinia.
OX NCBI_TaxID=5180;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W2-A4-4;
RX MEDLINE=21247026; PubMed=11348503;
RA Carbone I., Kohn L.M.;
RT "A microbial population-species interface: nested cladistic and
RT coalescent inference with multilocus data.";
RL Mol. Ecol. 10:947-964(2001).
DR EMBL; AF340959; AAK09778.1; -.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; F:structural constituent of cytoskeleton; IEA.
DR Pfam; PF00022; Actin; 1.
FT NON TER 1
SQ SEQUENCE 20 AA; 2141 MW; B06CCBB097FA4ABD CRC64;

Query Match 100.0%; Score 80; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRAVFPSIVGRPRH 15
DB 4 APRAVFPSIVGRPRH 18

RESULT 13
Q9C229
ID Q9C229 PRELIMINARY; PRT; 20 AA.
AC Q9C229;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Actin (Fragment).
GN Name=act;
OS Sclerotinia sclerotiorum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomyces;
OC Helotiales; Sclerotiniaceae; Sclerotinia.
OX NCBI_TaxID=5180;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W2-A3-5;
RX MEDLINE=21247026; PubMed=11348503;
RA Carbone I., Kohn L.M.;
RT "A microbial population-species interface: nested cladistic and
RT coalescent inference with multilocus data.";
RL Mol. Ecol. 10:947-964(2001).
DR EMBL; AF340958; AAK09777.1; -.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; F:structural constituent of cytoskeleton; IEA.
DR Pfam; PF00022; Actin; 1.
FT NON TER 1
SQ SEQUENCE 20 AA; 2141 MW; B06CCBB097FA4ABD CRC64;

Query Match 100.0%; Score 80; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRAVFPSIVGRPRH 15
DB 4 APRAVFPSIVGRPRH 18

RESULT 14
Q9C300
ID Q9C300 PRELIMINARY; PRT; 20 AA.
AC Q9C300;

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Job time : 58.8667 secs

DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Actin (Fragment).
 GN Name=act;
 OS Sclerotinia sclerotiorum.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomyces;
 OC Helotiales; Sclerotiniaceae; Sclerotinia.
 OX NCBI_TaxID=5180;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=W2-A3-4;
 RX MEDLINE=21247026; PubMed=11348503;
 RA Carbone I., Kohn L.M.;
 RT "A microbial population-species interface: nested cladistic and
 RL coalescent inference with multilocus data.";
 RL Mol. Ecol. 10:947-964(2001).
 DR EMBL; AF340957; AAK09776.1;
 DR GO; GO:0015629; C:actin cytoskeleton; IEA.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
 DR InterPro; IPR004000; Actin_like.
 DR Pfam; PF00022; Actin; 1.
 FT NON_TER 1
 SQ SEQUENCE 20 AA; 2141 MW; B06CCBB097FA4ABD CRC64;

Query Match 100.0%; Score 80; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.2e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRAVFPSIVGRPRH 15
 Db |||||
 4 APRAVFPSIVGRPRH 18

RESULT 15

ID Q9C301 PRELIMINARY; PRT; 20 AA.
 AC Q9C301;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Actin (Fragment).
 GN Name=act;
 OS Sclerotinia sclerotiorum.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomyces;
 OC Helotiales; Sclerotiniaceae; Sclerotinia.
 OX NCBI_TaxID=5180;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=W1-A5-4;
 RX MEDLINE=21247026; PubMed=11348503;
 RA Carbone I., Kohn L.M.;
 RT "A microbial population-species interface: nested cladistic and
 RL coalescent inference with multilocus data.";
 RL Mol. Ecol. 10:947-964(2001).
 DR EMBL; AF340956; AAK09775.1;
 DR GO; GO:0015629; C:actin cytoskeleton; IEA.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
 DR InterPro; IPR004000; Actin_like.
 DR Pfam; PF00022; Actin; 1.
 FT NON_TER 1
 SQ SEQUENCE 20 AA; 2141 MW; B06CCBB097FA4ABD CRC64;

Query Match 100.0%; Score 80; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.2e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRAVFPSIVGRPRH 15
 Db |||||
 4 APRAVFPSIVGRPRH 18

Search completed: April 8, 2005, 12:03:04

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 62.4 Seconds
(without alignments)
92.971 Million cell updates/sec

Title: US-09-423-351C-2

Perfect score: 80

Sequence: 1 FPSIVGRPRHQGVNV 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	80	100.0	15	2 AAW92528	Beta-acti
2	80	100.0	105	5 ABP42469	Abp42469 Human ova
3	80	100.0	157	4 ABB66853	Abb66853 Drosophil
4	80	100.0	201	5 ABP43176	Abp43176 Human ova
5	80	100.0	204	5 ABP43016	Abp43016 Human ova
6	80	100.0	310	8 ADR38362	Adr38362 pigA3Cy3G
7	80	100.0	342	7 ADM05323	Adm05323 Human pro
8	80	100.0	374	3 AAB12985	Aab12985 Human bet
9	80	100.0	375	1 AAP61532	Aap61532 Sequence
10	80	100.0	375	2 AAR50328	Aar50328 Drug resi
11	80	100.0	375	3 AAB15017	Aab15017 Posttrans
12	80	100.0	375	3 AAY94569	Aay94569 Human car
13	80	100.0	375	3 AAB15016	Aab15016 Posttrans
14	80	100.0	375	5 ABB77395	Abb77395 Human act
15	80	100.0	375	6 ABR64321	AbR64321 Angiogene
16	80	100.0	375	6 ABM04830	Abm04830 Rat cytop
17	80	100.0	375	7 ADB85212	AdB85212 Rat actin
18	80	100.0	375	7 ADB61174	AdB61174 Rat Prote
19	80	100.0	375	7 ADF30525	AdF30525 Rat angio
20	80	100.0	375	7 ADI63062	AdI63062 Human apo
21	80	100.0	375	7 ADI62970	AdI62970 Human apo
22	80	100.0	375	7 ADI63040	AdI63040 Human apo
23	80	100.0	375	8 ADL13002	AdL13002 Human ste
24	80	100.0	375	8 ADJ78489	AdJ78489 Actin pro
25	80	100.0	375	8 ADL14103	AdL14103 Human sar

26	80	100.0	375	8 ADP04899	Adp04899 Sea squir
27	80	100.0	375	8 ADP12391	Adp12391 Protein e
28	80	100.0	375	8 ADQ26098	Adq26098 Gamma 1 a
29	80	100.0	375	8 ABO84772	AbO84772 Human can
30	80	100.0	375	8 ABM80841	Abm80841 Tumour-as
31	80	100.0	375	8 ADN23274	Adn23274 Bacterial
32	80	100.0	375	8 ADS88828	AdS88828 Amino aci
33	80	100.0	375	8 ADS88825	AdS88825 Amino aci
34	80	100.0	375	8 ADS88826	AdS88826 Amino aci
35	80	100.0	375	8 ADS88827	AdS88827 Amino aci
36	80	100.0	375	2 AAW19799	Aaw19799 Gamma-smo
37	80	100.0	376	4 ABB58162	Abb58162 Drosophil
38	80	100.0	376	4 ABB61322	Abb61322 Drosophil
39	80	100.0	376	4 ABB60354	Abb60354 Drosophil
40	80	100.0	376	4 ABB64853	Abb64853 Drosophil
41	80	100.0	376	4 ABB63315	Abb63315 Drosophil
42	80	100.0	376	6 ABR62327	AbR62327 Pacific w
43	80	100.0	376	8 ADN03845	Adn03845 Antipsoi
44	80	100.0	377	3 AAB15014	Aab15014 Human car
45	80	100.0	377	3 AAY94568	Aay94568 Human car

ALIGNMENTS

RESULT 1
AAW92528
ID AAW92528 standard; peptide; 15 AA.
XX
AC AAW92528;
XX
DT 26-APR-1999 (first entry)
XX
DE Beta-actin reference peptide substrate #2.
XX
KW Peptide substrate; CCT; eukaryotic type II chaperonin complex; cyclin;
KW binding agent; substrate-binding site; SBS; substrate folding; actin;
KW tubulin; treatment; cancer; anticancer drug; viral infection; screening;
KW reduced toxicity.
XX
OS Synthetic.
XX
PN WO9853322-Al.
XX
PD 26-NOV-1998.
XX
PF 22-MAY-1998; 98WO-GB001485.
XX
PR 23-MAY-1997; 97GB-00010762.
XX
(CANC-) INST CANCER RES ROYAL CANCER HOSPITAL.
XX
Willison K, Hynes G, Liou AK;
WPI; 1999-070162/06.
Identifying specific binding agents for substrate binding site in CCT
chaperonin complex - also new peptide binding agents and their mimetics,
and peptides containing a specific CCT binding site, used for treating
cancer.
Disclosure; Fig 10; 97pp; English.

This invention describes a method which uses the CCT (eukaryotic type II chaperonin) complex or part of it, for identifying a binding agent that can occupy a substrate-binding site (SBS) on the CCT complex. By binding to the CCT complex, the binding agents block an SBS so that biological activity of the CCT complex is affected, particularly its ability to fold substrates such as actin, tubulin and cyclin. The binding agents are useful for treatment of cancer, particularly when used in combination with an anticancer drug, or viral infections. Nucleic acid fragments are used to screen for agents, e.g. binding agents that modulate interaction between the CCT complex and a protein that is to be folded. The binding

CC agents may target cells that are actively synthesizing tubulin etc.
 CC (unlike known microtubule-stabilising agents that affect all cells), so
 CC should have reduced toxicity for normal cells. AAM92527-W92541 are
 CC peptide substrates used in the method of the invention
 XX
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 80; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.1e-07; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0;
 XX
 QY 1 FPSIVGRPRHQGVWV 15
 |||||
 DB 1 FPSIVGRPRHQGVWV 15
 |||||
 RESULT 2
 ID ABP42469 standard; protein; 105 AA.
 XX
 AC ABP42469;
 XX
 DT 22-AUG-2002 (first entry)
 XX
 DE Human ovarian antigen HOCQ94, SEQ ID NO:3601.
 XX
 KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive.
 XX
 OS Homo sapiens.
 XX
 PN WO200200677-A1.
 XX
 PD 03-JAN-2002.
 XX
 PF 07-JUN-2001; 2001WO-US018569.
 XX
 PR 07-JUN-2000; 2000US-0209467P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Birse CE, Rosen CA;
 XX
 DR WPI, 2002-147878/19.
 DR N-PSDB; ABQ55346.
 XX
 PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 PT cancer), immune disorders, cardiovascular disorders and neurological
 PT diseases.
 XX
 PS Claim 11; SEQ ID NO 3601; 2922pp; English.
 XX
 CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovary and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine

CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 105 AA;
 Query Match 100.0%; Score 80; DB 5; Length 105;
 Best Local Similarity 100.0%; Pred. No. 3.9e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FPSIVGRPRHQGVWV 15
 |||||
 DB 32 FPSIVGRPRHQGVWV 46
 |||||
 RESULT 3
 ID ABB66853 standard; protein; 157 AA.
 XX
 AC ABB66853;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 27351.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US009231.
 XX
 PR 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI, 2001-656860/75.
 DR N-PSDB; ABL10956.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 XX
 PS Disclosure; SEQ ID NO 27351; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-

CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 157 AA;
Query Match 100.0%; Score 80; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 5.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FPSIVGRPRHQGVWV 15
Db 32 FPSIVGRPRHQGVWV 46
RESULT 4
ABP43176
ID ABP43176 standard; protein; 201 AA.
AC
XX
AC ABP43176;
XX
DT 22-AUG-2002 (first entry)
XX
DE Human ovarian antigen HVVQ049, SEQ ID NO:4308.
XX
XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive.
XX
OS Homo sapiens.
XX
XX WO200200677-A1.
XX
XX
XX 03-JAN-2002.
XX
XX 07-JUN-2001; 2001WO-US018569.
XX
XX 07-JUN-2000; 2000US-0209467P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Birse CE, Rosen CA;
XX
XX WPI; 2002-147878/19.
XX N-PSDB; ABQ56253.
XX
XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
XX useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
XX cancer), immune disorders, cardiovascular disorders and neurological
XX diseases.
XX
XX Claim 11; SEQ ID NO 4308; 2922pp; English.
XX
XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
XX ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
XX encompasses polypeptides 90% identical and polynucleotides 95% identical
XX to the sequences of the invention. The invention additionally relates to
XX recombinant vectors and host cells comprising human ovarian antigen
XX polynucleotides, antibodies against human ovarian antigens, and the use
XX of ovarian antigen polynucleotides and polypeptides in diagnosing,
XX treating, prognosing or preventing various ovary and/or breast-related
XX disorders. Such conditions include ovarian cancer and breast cancer, and
XX metastatic tumours of ovarian or breast origin, reproductive system
XX disorders (e.g., infertility, disorders of pregnancy, anovulation,
XX polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
XX disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic

CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a human ovarian antigen of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 201 AA;
Query Match 100.0%; Score 80; DB 5; Length 201;
Best Local Similarity 100.0%; Pred. No. 7.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FPSIVGRPRHQGVWV 15
Db 48 FPSIVGRPRHQGVWV 62
RESULT 5
ABP43016
ID ABP43016 standard; protein; 204 AA.
XX
AC ABP43016;
XX
XX 22-AUG-2002 (first entry)
XX
XX Human ovarian antigen HSPSB24, SEQ ID NO:4148.
XX
XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive.
XX
XX Homo sapiens.
XX
XX WO200200677-A1.
XX
XX 03-JAN-2002.
XX
XX 07-JUN-2001; 2001WO-US018569.
XX
XX 07-JUN-2000; 2000US-0209467P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Birse CE, Rosen CA;
XX
XX WPI; 2002-147878/19.
XX N-PSDB; ABQ56093.
XX
XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
XX useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
XX cancer), immune disorders, cardiovascular disorders and neurological
XX diseases.
XX
XX Claim 11; SEQ ID NO 4148; 2922pp; English.
XX
XX

CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovary and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 204 AA;

Query Match 100.0%; Score 80; DB 5; Length 204;
 Best Local Similarity 100.0%; Pred. No. 7.8e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPSIVGRPRHQGVWV 15
 |||||
 DB 51 FPSIVGRPRHQGVWV 65

RESULT 6

ADR38362
 ID ADR38362 standard; protein; 310 AA.

XX
 AC ADR38362;

XX 18-NOV-2004 (first entry)

XX pigA3Cy3GFP plasmid protein product (Cycle3 GFP under an actin promoter).

XX piggyBac; transposon; transposase; gene transfer; plasmid; Cycle3 GFP;
 KW actin promoter.

XX Bombyx mori.

OS Synthetic.

OS Unidentified.

XX Key Location/Qualifiers

FT Misc-difference 20 /note= "Encoded by GCC"

XX JP2004236642-A.

XX 26-AUG-2004.

XX 10-FEB-2003; 2003JP-00032306.

XX 10-FEB-2003; 2003JP-00032306.

XX (TORA) TORAY IND INC.

XX WPI; 2004-608233/59.

DR N-PSDB; ADR38361.

XX Introducing foreign gene into insect cell, involves introducing DNA
 PT having foreign gene integrated between inverted repeat sequences of
 PT piggyBac transposon and piggyBac transposase that acts on inverted repeat
 PT sequence.

XX Disclosure; Page; 25pp; Japanese.

XX This invention relates to a novel method for introducing a foreign gene
 CC into an insect cell. Specifically, it refers to a foreign gene occurring
 CC between inverted repeat sequences of a piggyBac transposon and using a
 CC piggyBac transposase for gene transfer to give a high recombinant
 CC efficiency. The present invention describes the insect cell as that of
 CC Lepidoptera insect origin, preferably it is the silk worm Bombyx mori,
 CC and stable integration occurs into the genome of this insect using the
 CC transposase enzyme. In particular, this gene transfer method uses the
 CC plasmid pigA3Cy3GFP which contains a Cycle3 GFP gene expressed under a
 CC silk worm actin promoter (A3 promoter) between a pair of inverted repeat
 CC sequences of the transposon piggyBac. This polypeptide sequence is the
 CC protein product from the pigA3Cy3GFP plasmid DNA that represents the
 CC silkworm actin promoter controlling expression of the Cycle3 GFP gene
 CC given in an exemplification of the invention. NOTE: This sequence is
 CC given as an embedded protein in the sequence listing and is not referred
 CC to further within the specification.

XX Sequence 310 AA;

Query Match 100.0%; Score 80; DB 8; Length 310;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPSIVGRPRHQGVWV 15

DB 32 FPSIVGRPRHQGVWV 46
 |||||

RESULT 7

ADM05323
 ID ADM05323 standard; protein; 342 AA.

XX
 AC ADM05323;

XX 20-MAY-2004 (first entry)

XX Human protein of the invention SEQ ID NO:4008.

XX human; gene therapy; diagnostic marker; pharmaceutical.

XX Homo sapiens.

XX EPI347046-A1.

XX 24-SEP-2003.

XX 12-APR-2002; 2002EP-00008400.

XX 22-MAR-2002; 2002JP-00137785.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;

XX Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;

XX Seki N, Yoshikawa T, Otsuka M, Nagahari K, Maeuho Y;

XX WPI; 2003-723558/69.

XX N-PSDB; ADM02880.

XX New polynucleotides and polypeptides are useful in gene therapy, for
 PT developing a diagnostic marker or medicines for regulating their
 PT expression and activity, or as a target of gene therapy.

XX Claim 1; SEQ ID NO 4008; 305pp; English.

XX The invention relates to a novel human polynucleotide and the encoded
 CC polypeptide. A polynucleotide of the invention may have a use in gene
 CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
 CC as a primer for synthesizing the polynucleotide or as a probe for
 CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
 CC useful in gene therapy, for developing a diagnostic marker or medicines
 CC for regulating their expression and activity, or as a target of gene
 CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
 CC are useful as pharmaceutical agents. The present sequence represents a
 CC protein sequence of the invention.
 XX
 XX Sequence 342 AA;
 SQ
 Query Match 100.0%; Score 80; DB 7; Length 342;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 15; Conservative 0;
 QY 1 FPSIVGRPRHQGMV 15
 |||||
 DB 33 FPSIVGRPRHQGMV 47
 |||||
 RESULT 8
 AAB12985
 ID AAB12985 standard; protein; 374 AA.
 XX
 AC AAB12985;
 XX
 DT 29-NOV-2000 (first entry)
 XX
 DE Human beta-actin protein sequence.
 XX
 KW Beta actin; post translational modification; sickle cell anaemia;
 KW irreversibly sickled cell; ISC; treatment.
 XX
 OS Homo sapiens.
 XX
 FN US6087398-A.
 XX
 PD 11-JUL-2000.
 XX
 PF 01-MAR-1996; 96US-00609236.
 XX
 PR 14-AUG-1995; 95US-0002288P.
 XX
 PA (SALA-) SOUTH ALABAMA MEDICAL SCI FOUND.
 XX
 PI Goodman SR;
 XX
 DR WPI; 2000-498210/44.
 XX
 PT Treatment for sickle cell anemia comprises administering a reducing agent
 PT to inhibit and reverse sickled cell formation in blood.
 XX
 PS Example 17; Fig 5B; 53pp; English.
 XX
 CC This invention provides a treatment for sickle cell anaemia, which
 CC comprises administering a reducing agent. The treatment inhibits the
 CC formation of irreversibly sickled cells (ISC) and reverses ISC formation
 CC in the blood. The present sequence represents the human beta-actin
 CC protein. The sequence is used in the invention to demonstrate that a
 CC disulphide bridge is formed between cysteines 284 and 373 in ISC beta-
 CC actin as a post-translational modification. The reducing agent used in
 CC the treatment acts to correct this post-translational modification
 XX
 SQ Sequence 374 AA;
 Query Match 100.0%; Score 80; DB 3; Length 374;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FPSIVGRPRHQGMV 15
 |||||

DB 30 FPSIVGRPRHQGMV 44
 |||||
 RESULT 9
 AAP61532
 ID AAP61532 standard; protein; 375 AA.
 XX
 AC AAP61532;
 XX
 DT 25-MAR-2003 (revised)
 DT 13-SEP-1991 (first entry)
 XX
 DE Sequence of beta-actin.
 XX
 KW Actin fibre; actin film; recombinant beta-actin.
 XX
 OS Homo sapiens.
 XX
 PN EP174608-A.
 XX
 PD 19-MAR-1986.
 XX
 PF 05-SEP-1985; 85EP-00111225.
 XX
 PR 13-SEP-1984; 84US-00650958.
 XX
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 XX
 PI Leavitt JC, Kedes LH, Gunning PW;
 XX
 DR WPI; 1986-077015/12.
 DR N-PSDB; AAN60172.
 XX
 PT Beta-actin gene and regulatory elements - used for expression of
 PT polypeptide(s) in mammalian host cells.
 XX
 PS Example; Page 23-24; 32pp; English.
 XX
 CC In the example, a beta-actin expression vector providing the beta- actin
 CC promoter region, a polylinker and a polyadenylation signal was
 CC constructed where the expression construct was present on a vector having
 CC a bacterial origin of replication, as well as a marker for selection in a
 CC mammalian host. (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 375 AA;
 Query Match 100.0%; Score 80; DB 1; Length 375;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FPSIVGRPRHQGMV 15
 |||||
 DB 31 FPSIVGRPRHQGMV 45
 |||||
 RESULT 10
 AAR50328
 ID AAR50328 standard; protein; 375 AA.
 XX
 AC AAR50328;
 XX
 DT 12-OCT-1994 (first entry)
 XX
 DE Drug resistant structural protein.
 XX
 KW Drug resistant; structural gene; expression vector; selective; marker;
 KW transformation; thymidine-kinase deleted cell.
 XX
 OS Homo sapiens.
 XX
 PN JP06038773-A.
 XX

PD 15-FEB-1994.
 XX
 XX 31-JAN-1992; 92JP-00045939.
 XX
 XX 31-JAN-1992; 92JP-00045939.
 XX (TOVM) TOYOBO KK.
 XX WPI; 1994-094836/12.
 DR N-PSDB; AAA44861.
 XX
 XX Expression vector contg. drug resistant marker gene - useful for
 PT transformation of thymidine kinase-deleted human cells for high levels of
 PT foreign protein prodn.
 XX
 XX Disclosure; Page 5-7; 7pp; Japanese.
 XX
 XX This sequence is encoded by a drug resistant structural gene which may be
 CC used in the expression vector of the invention. This gene is used as the
 CC selective marker in the vector. The resulting vector may be used to
 CC transform a thymidine-kinase deleted cell allowing introduction of a
 CC foreign structural gene. The transformed cell may be used to produce
 CC large amounts of useful protein
 XX
 XX Sequence 375 AA;
 SQ
 Query Match 100.0%; Score 80; DB 2; Length 375;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FPSIVGRPRHOGVMV 15
 DB 31 FPSIVGRPRHOGVMV 45
 |||||
 RESULT 11
 AAB15017
 ID AAB15017 standard; protein; 375 AA.
 XX
 AC AAB15017;
 XX
 DT 07-DEC-2000 (first entry)
 XX
 DE Posttranslationally modified human cardiac actin mutant E361G.
 XX
 XX Cardiac actin; ACTC; human; gene therapy; IDC; chromosome 15q14;
 KW idiopathic dilated cardiomyopathy; mutant; mutein.
 XX
 XX Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 361
 FT /note= "Wild-type Glu substituted by Gly"
 XX
 XX US06063576-A.
 PN
 XX 16-MAY-2000.
 PD
 XX 29-JUN-1998; 98US-00106217.
 PF
 XX 29-JUN-1998; 98US-00106217.
 PR
 XX (UTAH) UNIV UTAH RES FOUND.
 PA
 XX Olson TM, Keating MT;
 PI
 XX WPI; 2000-375488/32.
 DR N-PSDB; AAA73739.
 XX
 XX New cardiac actin gene comprising histidine to arginine or glycine to
 PT glutamic acid substitution, useful in the diagnosis of diseases
 PT associated with the mutation, specifically idiopathic dilated

cardiomyopathy.
 PT
 XX Claim 3; Page; 36pp; English.
 PS
 XX The present invention relates to human cardiac actin (ACTC). Genotypic
 CC analyses show that ACTC is linked to idiopathic dilated cardiomyopathy
 CC (IDC). The ACTC gene maps to chromosome 15q14. Six PCR primer pairs
 CC (AAA49020 to AAA49031) have been developed to allow analysis of the six
 CC exons of ACTC. Studies of two families with IDC showed the presence of
 CC two mutations, one in exon 5 and one in exon 6. The present sequence is a
 CC mutant of posttranslationally modified ACTC without the initial two
 CC residues. The mutation is a Glu to Gly mutation at position 361. The ACTC
 CC protein may be used in a variety of methods for drug screening and for
 CC rational drug design. The ACTC gene may be used to treat IDC by gene
 CC therapy. Analysis of the ACTC gene provides early identification of
 CC subjects likely to develop or who already have IDC. Note: The present
 CC sequence is not shown in the specification but is derived from the ACTC
 CC sequence described in AAY94569
 XX
 XX Sequence 375 AA;
 SQ
 Query Match 100.0%; Score 80; DB 3; Length 375;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FPSIVGRPRHOGVMV 15
 DB 31 FPSIVGRPRHOGVMV 45
 |||||
 RESULT 12
 AAY94569
 ID AAY94569 standard; protein; 375 AA.
 XX
 AC AAY94569;
 XX
 DT 07-DEC-2000 (first entry)
 XX
 DE Human cardiac actin protein after posttranslational modification.
 XX
 XX Cardiac actin; ACTC; human; gene therapy; IDC; 15q14;
 KW idiopathic dilated cardiomyopathy.
 XX
 XX Homo sapiens.
 OS
 XX US06063576-A.
 PN
 XX 16-MAY-2000.
 PD
 XX 29-JUN-1998; 98US-00106217.
 PF
 XX 29-JUN-1998; 98US-00106217.
 PR
 XX (UTAH) UNIV UTAH RES FOUND.
 PA
 XX Olson TM, Keating MT;
 PI
 XX WPI; 2000-375488/32.
 DR N-PSDB; AAA49032.
 XX
 XX New cardiac actin gene comprising histidine to arginine or glycine to
 PT glutamic acid substitution, useful in the diagnosis of diseases
 PT associated with the mutation, specifically idiopathic dilated
 PT cardiomyopathy.
 XX
 XX Claim 3; Col 61-62; 36pp; English.
 PS
 XX The present sequence is human cardiac actin (ACTC) protein, without the
 CC initial Met-Cys which is posttranslationally removed. Genotypic analyses
 CC show that ACTC is linked to idiopathic dilated cardiomyopathy (IDC). The
 CC ACTC gene maps to chromosome 15q14. Six PCR primer pairs (AAA49020 to
 CC AAA49031) have been developed to allow analysis of the six exons of ACTC.
 CC Studies of two families with IDC showed the presence of two mutations,

CC one in exon 5 and one in exon 6. The mutations are G to A in codon 312
CC (Arg312His) and A to G in codon 361 (Glu361Gly). The ACTC protein may be
CC used in a variety of methods for drug screening and for rational drug
CC design. The ACTC gene may be used to treat IDC by gene therapy. Analysis
CC of the ACTC gene provides early identification of subjects likely to
CC develop or who already have IDC
XX
SQ Sequence 375 AA;

Query Match 100.0%; Score 80; DB 3; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHOGVMV 15
Db 31 FPSIVGRPRHOGVMV 45

RESULT 13
AAB15016
ID AAB15016 standard; protein; 375 AA.

AC AAB15016;

DT 07-DEC-2000 (first entry)

DE Posttranslationally modified human cardiac actin mutant R312H.

XX Cardiac actin; ACTC; human; gene therapy; IDC; chromosome 15q14;

KW idiopathic dilated cardiomyopathy; mutant; mutein.

XX Homo sapiens.

OS Synthetic.

FH Key Location/Qualifiers

FT Misc-difference 312
FT /note= "Wild-type Arg substituted by His"

XX US6063576-A.

XX 16-MAY-2000.

PF 29-JUN-1998; 98US-00106217.

PR 29-JUN-1998; 98US-00106217.

XX (UTAH) UNIV UTAH RES FOUND.

XX Olson TM, Keating MT;

XX WPI; 2000-375488/32.

DR N-PSDB; AAB73738.

XX New cardiac actin gene comprising histidine to arginine or glycine to
PT glutamic acid substitution, useful in the diagnosis of diseases
PT associated with the mutation, specifically idiopathic dilated
PT cardiomyopathy.

PS Claim 3; Page; 36pp; English.

XX The present invention relates to human cardiac actin (ACTC). Genotypic
CC analyses show that ACTC is linked to idiopathic dilated cardiomyopathy
CC (IDC). The ACTC gene maps to chromosome 15q14. Six PCR primer pairs
CC (AAA49020 to AAA49031) have been developed to allow analysis of the six
CC exons of ACTC. Studies of two families with IDC showed the presence of
CC two mutations, one in exon 5 and one in exon 6. The present sequence is a
CC mutant of posttranslationally modified ACTC without the initial two
CC residues. The mutation is Arg to His mutation at position 312. The ACTC
CC protein may be used in a variety of methods for drug screening and for
CC rational drug design. The ACTC gene may be used to treat IDC by gene
CC therapy. Analysis of the ACTC gene provides early identification of
CC subjects likely to develop or who already have IDC. Note: The present
CC sequence is not shown in the specification but is derived from the ACTC

CC sequence described in AAY94569

XX Sequence 375 AA;

Query Match 100.0%; Score 80; DB 3; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHOGVMV 15
Db 31 FPSIVGRPRHOGVMV 45

RESULT 14
ABB77395
ID ABB77395 standard; protein; 375 AA.

XX ABB77395;

DT 11-JUL-2002 (first entry)

DE Human actin gamma 1.

XX Human; dermatological; skin stress; ageing; spondin 2; cathepsin L;
KW actin gamma 1; vimentin; fibroblast; skin; cosmetic; pharmaceutical.

XX Homo sapiens.

XX DE10050274-A1.

XX 18-APR-2002.

PF 09-OCT-2000; 2000DE-01050274.

PR 09-OCT-2000; 2000DE-01050274.

XX (HENK) HENKEL KGAA.

XX Petersohn D, Schmitt G, Foerster T;

XX WPI; 2002-373046/41.

XX In vitro assays for skin stress and skin ageing includes determination of
PT spondin 2, cathepsin L, actin gamma 1 and vimentin fragments secreted by
PT skin fibroblasts.

PS Claim 6; Page 12; 14pp; German.

XX The invention relates to in vitro methods for the detection of skin
CC stress and/or skin ageing in humans and animals based on the
CC determination of spondin 2, cathepsin L, actin gamma 1 or vimentin
CC fragments secreted by fibroblast from the skin under test. Use of the
CC methods in a test for potential cosmetics and pharmaceuticals with an
CC effect on these skin conditions and products containing vimentin
CC fragments are also included. Products containing vimentin fragments are
CC effective in the regulation, especially maintenance, of skin homeostasis

XX Sequence 375 AA;

Query Match 100.0%; Score 80; DB 5; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHOGVMV 15
Db 31 FPSIVGRPRHOGVMV 45

RESULT 15

ABR64271
ID ABR64271 standard; protein; 375 AA.

XX ABR64271;

XX	15-OCT-2003	(first entry)
DT	Angiogenesis protein BNO369.	
XX		
DE	Cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;	
XX	antipsoriatic; antiarteriosclerotic; cardiant; vasotropic; angiogenesis;	
XX	gene therapy; vasculature; cancer; rheumatoid arthritis; psoriasis;	
KW	diabetic retinopathy; cardiovascular disease; atherosclerosis;	
KW	ischemic limb disease; coronary artery disease.	
XX		
OS	Homo sapiens.	
XX		
XX	WO2003027285-A1.	
XX		
XX	03-APR-2003.	
PD		
XX		
PF	19-SEP-2002; 2002WO-AU001282.	
XX		
XX	27-SEP-2001; 2001AU-00007973.	
PR		
PR	27-SEP-2001; 2001AU-00007974.	
PR		
PR	11-OCT-2001; 2001AU-00008210.	
PR		
PR	23-OCT-2001; 2001AU-00008532.	
PR		
PR	13-NOV-2001; 2001AU-00008838.	
PR		
PR	28-AUG-2002; 2002AU-00951032.	
XX		
PA	(BION-) BIONOMICS LTD.	
XX		
PI	Gamble JR, Hahn CN, Vadas MA;	
XX		
XX	WPI; 2003-354655/33.	
DR		
DR	N-PSDB; ACF34548.	
XX		
XX	New angiogenic genes and polypeptides, useful for diagnosing,	
PT	prognosticating or treating an angiogenesis-related disorder, e.g.	
PT	cancer, rheumatoid arthritis, diabetic retinopathy, psoriasis or	
PT	cardiovascular diseases.	
XX		
XX	Claim 15; SEQ ID NO 206; 90pp; English.	
XX		
CC	The invention relates to the isolation of novel genes (ACF34446-ACF34559)	
CC	encoding proteins (ABR64180-ABR64281) involved in the process of	
CC	angiogenesis. The nucleic acid molecules are useful in identifying and/or	
CC	obtaining full-length human genes involved in an angiogenic process. The	
CC	nucleic acid molecule, polypeptides or complexes encoded, cells or	
CC	genetically modified non-human animals derived from these are useful for	
CC	the screening of candidate pharmaceutical compounds used in treating	
CC	angiogenesis-related disorders. They are also useful for diagnosing,	
CC	prognosticating or treating an angiogenesis-related disorder, which	
CC	involves uncontrolled or enhanced angiogenesis or is a disorder in which	
CC	a decreased vasculature is of benefit (e.g. cancer, rheumatoid arthritis,	
CC	diabetic retinopathy, psoriasis or cardiovascular diseases such as	
CC	atherosclerosis), or involves inappropriately arrested or decreased	
CC	angiogenesis or is a disorder in which an expanding vasculature is of	
CC	benefit (e.g. ischemic limb disease or coronary artery disease). The	
CC	modulator of expression or activity of the polypeptide encoded by the	
CC	nucleic acid sequence is useful for manufacturing a medicament for the	
CC	treatment of an angiogenesis-related disorder. This sequence corresponds	
CC	to one of the novel angiogenic protein	
XX		
XX	Sequence 375 AA;	
XX		

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run On: April 8, 2005, 09:58:57 ; Search time 17.5333 Seconds
(without alignments)
63.863 Million cell updates/sec

Title: US-09-423-351C-2

Perfect score: 80

Sequence: 1 FPSIVGRPRHQGVVW 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	80	100.0	374	3	US-08-609-236-6
2	80	100.0	375	2	US-08-494-151-14
3	80	100.0	375	3	US-09-106-217-16
4	80	100.0	375	4	US-09-976-594-731
5	80	100.0	376	1	US-08-588-113-2
6	80	100.0	376	4	US-09-949-016-6100
7	80	100.0	377	3	US-09-106-217-2
8	80	100.0	377	4	US-09-919-172-33
9	80	100.0	377	4	US-09-917-254-53
10	80	100.0	386	4	US-09-949-016-7721
11	80	100.0	399	4	US-09-949-016-9424
12	80	100.0	402	4	US-09-949-016-10757
13	80	100.0	404	4	US-09-949-016-11313
14	77	96.2	377	4	US-09-248-796A-14109
15	75	93.8	71	4	US-09-621-976-6521
16	74	92.5	20	3	US-08-505-250-17
17	74	92.5	20	3	US-08-505-250-17
18	74	92.5	374	3	US-09-306-446C-2
19	73	91.2	375	3	US-09-171-337A-7
20	73	91.2	375	3	US-09-171-337A-8
21	73	91.2	375	4	US-09-631-022-7
22	73	91.2	375	4	US-09-631-022-8
23	55	68.8	41	3	US-09-306-446C-3
24	52	65.0	376	4	US-09-538-092-1110
25	52	65.0	376	4	US-09-949-016-6656
26	52	65.0	376	4	US-09-949-016-8452
27	50	62.5	362	4	US-09-949-016-7725

28 50 62.5 376 4 US-09-538-092-1109 Sequence 1109, Ap
29 48 60.0 11 4 US-09-786-066-5 Sequence 5, Appl
30 47 58.8 504 4 US-09-554-726A-10 Sequence 10, Appl
31 42 52.5 180 4 US-09-252-991A-31563 Sequence 31563, A
32 41 51.2 85 4 US-09-248-796A-18932 Sequence 18932, A
33 40 50.0 78 4 US-09-621-976-5181 Sequence 5181, Ap
34 40 50.0 212 4 US-09-252-991A-29187 Sequence 29187, A
35 39 48.8 150 4 US-09-732-210-626 Sequence 626, App
36 39 48.8 374 4 US-09-252-991A-28830 Sequence 28830, A
37 39 48.8 927 4 US-09-198-452A-472 Sequence 472, App
38 39 48.8 937 4 US-09-438-185A-449 Sequence 449, App
39 38 47.5 394 4 US-09-949-016-6655 Sequence 6655, Ap
40 38 47.5 406 4 US-09-949-016-7396 Sequence 7396, Ap
41 38 47.5 592 4 US-09-252-991A-22838 Sequence 22838, A
42 38 47.5 630 4 US-09-252-991A-26324 Sequence 26324, A
43 38 47.5 1220 1 US-08-158-232-43 Sequence 43, Appl
44 38 47.5 1220 2 US-08-611-928-43 Sequence 43, Appl
45 38 47.5 1220 3 US-09-173-891-43 Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-08-609-236-6
; Sequence 6, Application US/08609236
; Patent No, 6087398
; GENERAL INFORMATION:
; APPLICANT: Steven R. Goodman
; TITLE OF INVENTION: No. 6087398el Sickie Cell Anemia Treatment
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McGregor & Adler, LLP
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,236
; FILING DATE: March 1, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/002,288
; FILING DATE: August 14, 1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Benjamin Aaron Adler, Ph.D.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5807
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6908
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374
; TYPE: Amino acid
; STRANDEDNESS:
; TOPOLOGY: Linear
; MOLECULE TYPE:
; DESCRIPTION: Protein
; HYPOTHETICAL: No
; ANTI-SENSE: No
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:

TISSUE TYPE:
CELL TYPE:
CELL LINE:

US-08-609-236-6

Query Match 100.0%; Score 80; DB 3; Length 374;
Best Local Similarity 100.0%; Pred. No. 6.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHOGVMV 15
Db 30 FPSIVGRPRHOGVMV 44

RESULT 2

US-08-494-151-14
Sequence 14, Application US/08494151
Patent No. 5840528
GENERAL INFORMATION:
APPLICANT: Van Ooyen, Albert Johannes Joseph
TITLE OF INVENTION: Transformation of Phaffia rhodozyma
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: Morrison & Foerster
FILING DATE: 23-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20039.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-494-151-14

Query Match 100.0%; Score 80; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 6.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHOGVMV 15
Db 31 FPSIVGRPRHOGVMV 45

RESULT 3

US-09-106-217-16
Sequence 16, Application US/09106217
Patent No. 6063576
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Olson, Timothy M.
TITLE OF INVENTION: Actin Mutations in Dilated
TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:

ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
STREET: 555 Thirteenth Street, N.W., Suite 701 East
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106.217
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 2323-125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-783-6040
TELEFAX: 202-783-6031

INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-106-217-16

Query Match 100.0%; Score 80; DB 3; Length 375;
Best Local Similarity 100.0%; Pred. No. 6.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHOGVMV 15
Db 31 FPSIVGRPRHOGVMV 45

RESULT 4

US-09-976-594-731
Sequence 731, Application US/09976594
Patent No. 6673549
GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976.594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
SEQ ID NO 731
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673549 1837317CD1
US-09-976-594-731

Query Match 100.0%; Score 80; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 6.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHOGVMV 15
Db 31 FPSIVGRPRHOGVMV 45

RESULT 5

US-08-588-113-2
; Sequence 2, Application US/08588113
; Patent No. 5710003
; GENERAL INFORMATION:
; APPLICANT: McHugh, Kirk M.
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR DETERMINING
; TITLE OF INVENTION: MALIGNANCY OF SMOOTH MUSCLE TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5710003ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/588,113
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Ralph, Rebecca L.
; REGISTRATION NUMBER: 35,152
; REFERENCE/DOCKET NUMBER: TJU-1652
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 376 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-588-113-2

Query Match 100.0%; Score 80; DB 1; Length 376;
Best Local Similarity 100.0%; Pred. No. 6.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPSIVGRPRHQGMV 15
|||
DB 32 FPSIVGRPRHQGMV 46

RESULT 6

US-09-949-016-6100
; Sequence 6100, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6100
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Human

US-09-949-016-6100

Query Match 100.0%; Score 80; DB 4; Length 376;
Best Local Similarity 100.0%; Pred. No. 6.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FPSIVGRPRHQGMV 15
|||
DB 32 FPSIVGRPRHQGMV 46

RESULT 7

US-09-106-217-2
; Sequence 2, Application US/09106217
; Patent No. 6063576
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Olson, Timothy M.
; TITLE OF INVENTION: Actin Mutations in Dilated
; TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rochwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; STREET: Tower
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/106,217
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 2323-125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-106-217-2

Query Match 100.0%; Score 80; DB 3; Length 377;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPSIVGRPRHQGMV 15
|||
DB 33 FPSIVGRPRHQGMV 47

RESULT 8

US-09-919-172-33
; Sequence 33, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30

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; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 33
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 1709118CD1
US-09-919-172-33

Query Match      100.0%; Score 80; DB 4; Length 377;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FPSIVGRPRHQGVNV 15
Db      33 FPSIVGRPRHQGVNV 47

RESULT 9
US-09-917-254-53
; Sequence 53, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
; APPLICANT: Mutter, George
; APPLICANT: Baak, Jan
; TITLE OF INVENTION: Prognostic Classification of Breast Cancer
; FILE REFERENCE: B0801/7224(JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/222,093
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 53
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-917-254-53

Query Match      100.0%; Score 80; DB 4; Length 377;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FPSIVGRPRHQGVNV 15
Db      33 FPSIVGRPRHQGVNV 47

RESULT 10
US-09-949-016-7721
; Sequence 7721, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7721
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7721

Query Match      100.0%; Score 80; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 7.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FPSIVGRPRHQGVNV 15
Db      42 FPSIVGRPRHQGVNV 56

RESULT 11
US-09-949-016-9424
; Sequence 9424, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9424
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9424

Query Match      100.0%; Score 80; DB 4; Length 399;
Best Local Similarity 100.0%; Pred. No. 7.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FPSIVGRPRHQGVNV 15
Db      55 FPSIVGRPRHQGVNV 69

RESULT 12
US-09-949-016-10757
; Sequence 10757, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10757
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10757

Query Match      100.0%; Score 80; DB 4; Length 402;
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Best Local Similarity 100.0%; Pred. No. 7.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHQGMV 15
Db 58 FPSIVGRPRHQGMV 72

RESULT 13

US-09-949-016-11313
; Sequence 11313, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11313
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11313

Query Match 100.0%; Score 80; DB 4; Length 404;
Best Local Similarity 100.0%; Pred. No. 7.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHQGMV 15
Db 60 FPSIVGRPRHQGMV 74

RESULT 14

US-09-248-796A-14109
; Sequence 14109, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 14109
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-14109

Query Match 96.2%; Score 77; DB 4; Length 377;
Best Local Similarity 86.7%; Pred. No. 2.3e-05;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHQGMV 15
Db 33 FPSIVGRPRHQGMV 47

RESULT 15

US-09-621-976-6521
; Sequence 6521, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6521
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 62
; OTHER INFORMATION: Xaa = Ala, Ser
; NAME/KEY: UNSURE
; LOCATION: 43
; OTHER INFORMATION: Xaa = Leu, Val
US-09-621-976-6521

Query Match 93.8%; Score 75; DB 4; Length 71;
Best Local Similarity 93.3%; Pred. No. 8.4e-06;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHQGMV 15
Db 31 FPSIVGRPRHQGMV 45

Search completed: April 8, 2005, 12:07:34
Job time : 18.5333 secs

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OM protein - protein search, using sw model

Run on: April 8, 2005, 10:53:18 ; Search time 42.6667 Seconds
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Title: US-09-423-351C-2

Perfect score: 80
Sequence: 1 FPSIVGRPRHOGVMV 15

Scoring table: BLOSUM62
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Searched: 1418010 seqs, 331997259 residues

Total number of hits satisfying chosen parameters: 1418010

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	80	100.0	105	15 US-10-264-049-3601	Sequence 3601, Ap
2	80	100.0	142	15 US-10-424-599-184471	Sequence 184471, Ap
3	80	100.0	201	15 US-10-264-049-4308	Sequence 4308, Ap
4	80	100.0	204	15 US-10-264-049-4148	Sequence 4148, Ap
5	80	100.0	219	14 US-10-002-631C-56	Sequence 56, Appl
6	80	100.0	342	15 US-10-108-260A-4008	Sequence 4008, Ap
7	80	100.0	371	16 US-10-322-281-68	Sequence 68, Appl
8	80	100.0	375	14 US-10-205-194-93	Sequence 93, Appl
9	80	100.0	375	14 US-10-316-253-88	Sequence 88, Appl
10	80	100.0	375	15 US-10-369-493-5927	Sequence 5927, Ap
11	80	100.0	375	15 US-10-205-331-94	Sequence 94, Appl
12	80	100.0	375	15 US-10-260-708-82	Sequence 82, Appl
13	80	100.0	376	15 US-10-341-434-101	Sequence 101, Appl

14	80	100.0	377	9 US-09-919-172-33	Sequence 33, Appl
15	80	100.0	377	15 US-10-236-031B-64	Sequence 64, Appl
16	80	100.0	377	16 US-10-333-680-4	Sequence 4, Appl
17	80	100.0	398	16 US-10-322-281-63	Sequence 63, Appl
18	80	100.0	413	9 US-09-925-301-1436	Sequence 1436, Ap
19	79	98.8	375	15 US-10-369-493-1786	Sequence 1786, Ap
20	79	98.8	375	16 US-10-477-369-1	Sequence 1, Appl
21	75	93.8	219	14 US-10-029-386-32056	Sequence 32056, A
22	74	92.5	135	16 US-10-767-701-47318	Sequence 47318, A
23	74	92.5	136	15 US-10-424-599-280811	Sequence 280811, A
24	74	92.5	197	15 US-10-424-599-280810	Sequence 280810, A
25	74	92.5	208	15 US-10-424-599-282905	Sequence 282905, A
26	74	92.5	230	16 US-10-767-701-42770	Sequence 42770, A
27	74	92.5	347	15 US-10-424-599-283333	Sequence 283333, A
28	74	92.5	375	15 US-10-369-493-2436	Sequence 2436, Ap
29	74	92.5	376	16 US-10-437-963-179917	Sequence 179917, A
30	74	92.5	376	16 US-10-437-963-202420	Sequence 202420, A
31	74	92.5	376	16 US-10-767-701-45677	Sequence 45677, A
32	74	92.5	376	16 US-10-767-701-46090	Sequence 46090, A
33	74	92.5	377	14 US-10-338-777-52	Sequence 52, Appl
34	74	92.5	377	15 US-10-424-599-162009	Sequence 162009, A
35	74	92.5	377	15 US-10-424-599-222816	Sequence 222816, A
36	74	92.5	377	15 US-10-424-599-223492	Sequence 223492, A
37	74	92.5	377	15 US-10-424-599-283336	Sequence 283336, A
38	74	92.5	377	15 US-10-425-114-66124	Sequence 66124, A
39	74	92.5	377	16 US-10-437-963-121952	Sequence 121952, A
40	74	92.5	377	16 US-10-437-963-148877	Sequence 148877, A
41	74	92.5	377	16 US-10-437-963-198295	Sequence 198295, A
42	74	92.5	377	16 US-10-767-701-47239	Sequence 47239, A
43	74	92.5	378	15 US-10-425-114-36824	Sequence 36824, A
44	74	92.5	378	15 US-10-425-114-42317	Sequence 42317, A
45	74	92.5	378	15 US-10-425-114-52458	Sequence 52458, A

ALIGNMENTS

RESULT 1
US-10-264-049-3601
; Sequence 3601, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P4133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 3601
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (103)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-3601

Query Match 100.0%; Score 80; DB 15; Length 105;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FPSIVGRPRHOGVMV 15
Db 32 FPSIVGRPRHOGVMV 46

RESULT 2

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US-10-424-599-184471
; Sequence 184471, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 184471
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_137594C.1.pep
US-10-424-599-184471

Query Match          100.0%; Score 80; DB 15; Length 142;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPSIVGRPRHQGVV 15
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Db 40 FPSIVGRPRHQGVV 54

RESULT 3
US-10-264-049-4308
; Sequence 4308, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4308
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (135)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (136)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (140)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (143)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (144)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
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US-10-264-049-4308
; LOCATION: (145)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (151)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (159)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (172)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (174)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (180)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-4308

Query Match          100.0%; Score 80; DB 15; Length 201;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPSIVGRPRHQGVV 15
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Db 48 FPSIVGRPRHQGVV 62

RESULT 4
US-10-264-049-4148
; Sequence 4148, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4148
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (148)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (151)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (159)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (172)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (174)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (180)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-4148

Query Match          100.0%; Score 80; DB 15; Length 204;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPSIVGRPRHQGVV 15
   |||||
Db 51 FPSIVGRPRHQGVV 65

RESULT 5
US-10-002-631C-56
; Sequence 56, Application US/10002631C
; Publication No. US20030157486A1
; GENERAL INFORMATION:
; APPLICANT: Graff, Jonathon M.
; APPLICANT: Muenster, Matthew
; TITLE OF INVENTION: METHODS TO IDENTIFY SIGNAL SEQUENCES
; FILE REFERENCE: A34943 090495.0243
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; CURRENT APPLICATION NUMBER: US/10/002,631C
;
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/300,309
; PRIOR FILING DATE: 2001-06-21
;
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-631C-56

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Query Match      100.0%; Score 80; DB 14; Length 219;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 FPSIVGRPRHQGMV 15
|||
Db 58 FPSIVGRPRHQGMV 72

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RESULT 6
US-10-108-260A-4008
; Sequence 4008, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO US20040005560A1el full length cDNA

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Query Match      100.0%; Score 80; DB 15; Length 342;
Best Local Similarity 100.0%; Pred. No. 6.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 FPSIVGRPRHQVMV 15
db 33 FPSIVGRPRHQVMV 47

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RESULT 7
US-10-322-281-68
; Sequence 68, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-281-68

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Query Match	100.0%;	Score 80;	DB 16;	Length 371;
Best Local Similarity	100.0%;	Pred. No. 7.2e-05;		
Matches 15:	Conservative	0;	Mismatches	0;
	Indels	0;	Gaps	0;

QY 1 FPSIVGRPRHQGMV 15

Db 31 FPSIVGRHQGVNV 45

RESULT 8

US-10-205-194-93

; Sequence 93, Application US/10205194

; Publication No. US20030134301A1

; GENERAL INFORMATION:

; APPLICANT: Warner-Lambert Company

; APPLICANT: Lee, Kevin

; APPLICANT: Dixon, Alistair

; APPLICANT: Brooksbank, Robert

; APPLICANT: Dinrock, Robert

Query Match	100.0%;	Score 80;	DB 14;	Length 375;
Best Local Similarity	100.0%;	Pred. No. 7.2e-05;		
Matches 15;	Conservative	0;	Mismatches 0;	Indels 0;
				Gaps 0;

Qy 1 FPSIVGRPRHQGMV 15
|||
Db 31 FPSIVGRPRHQGMV 45

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RESULT 9
US-10-316-253-88
; Sequence 88, Application US/10316253
; Publication NO. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Grets, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-88

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Query Match	Score 80;	DB 14;	Length 375;
Best Local Similarity	100.0%;	Pred. No. 7.2e-05;	
Matches 15:	Conservative 0;	Mismatches 0;	Indels 0;
	Conservative 0;		Gaps 0;

Qy 1 FPSIVGRPRHQVMV 15
 |||||
Dh 31 FPSIVGRPRHQVMV 45

RESULT 10
US-10-369-493-5927

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; Sequence 5927, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5927
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5927

Query Match 100.0%; Score 80; DB 15; Length 375;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHQGVV 15
Db 31 FPSIVGRPRHQGVV 45

RESULT 11
US-10-203-331-94
; Sequence 94, Application US/10205331
; Publication No. US20040058326A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pinnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018199
; CURRENT APPLICATION NUMBER: US/10/205,331
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 94
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Cytoplasmic beta-actin
US-10-203-331-94

Query Match 100.0%; Score 80; DB 15; Length 375;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHQGVV 15
Db 31 FPSIVGRPRHQGVV 45

RESULT 12
US-10-260-708-82
; Sequence 82, Application US/10260708
; Publication No. US20040063101A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Lee, Sang-Yull
```

```
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: Human Sarcoma-Associated Antigens
; FILE REFERENCE: L00461/70138
; CURRENT APPLICATION NUMBER: US/10/260,708
; CURRENT FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 375
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-260-708-82

Query Match 100.0%; Score 80; DB 15; Length 375;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHQGVV 15
Db 31 FPSIVGRPRHQGVV 45

RESULT 13
US-10-341-434-101
; Sequence 101, Application US/10341434
; Publication No. US20030215835A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
; FILE REFERENCE: 9U 204 205 R1
; CURRENT APPLICATION NUMBER: US/10/341,434
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/348,164
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 60/348,119
; PRIOR FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-341-434-101

Query Match 100.0%; Score 80; DB 15; Length 376;
Best Local Similarity 100.0%; Pred. No. 7.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHQGVV 15
Db 32 FPSIVGRPRHQGVV 46

RESULT 14
US-09-919-172-33
; Sequence 33, Application US/09919172
; Patent No. US20020119463A1
; GENERAL INFORMATION:
; APPLICANT: Paris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 33
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020119463A1 1709118CD1
US-09-919-172-33

Query Match 100.0%; Score 80; DB 9; Length 377;
Best Local Similarity 100.0%; Pred. No. 7.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHQGMV 15
| | | | | | | | | | | | | | |
Db 33 FPSIVGRPRHQGMV 47

RESULT 15
US-10-236-031B-64
; Sequence 64, Application US/10236031B
; Publication No. US20030219760A1
; GENERAL INFORMATION:
; APPLICANT: Gordon, Gavin J.
; APPLICANT: Jensen, Roderick V.
; APPLICANT: Gullans, Steven R.
; APPLICANT: Bueno, Raphael
; TITLE OF INVENTION: Diagnostic and Prognostic Tests
; FILE REFERENCE: B00801/70265 (JRV/JAV)
; CURRENT APPLICATION NUMBER: US/10/236,031B
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/317,389
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/407,431
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-031B-64

Query Match 100.0%; Score 80; DB 15; Length 377;
Best Local Similarity 100.0%; Pred. No. 7.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHQGMV 15
| | | | | | | | | | | | | | |
Db 33 FPSIVGRPRHQGMV 47

Search completed: April 8, 2005, 12:50:57
Job time : 42.6667 secs

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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 9.33333 Seconds
(without alignments)
154.634 Million cell updates/sec

Title: US-09-423-351C-2
Perfect score: 80
Sequence: 1 FPSIVGRPRHOGVMV 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	80	100.0	86	2	A43616
2	80	100.0	137	2	A28258
3	80	100.0	158	2	I49465
4	80	100.0	213	2	A61043
5	80	100.0	308	2	A03000
6	80	100.0	328	2	S05430
7	80	100.0	349	2	B25819
8	80	100.0	362	2	A28559
9	80	100.0	374	1	ATBOB
10	80	100.0	374	1	A48324
11	80	100.0	374	2	JCS518
12	80	100.0	375	1	ATBOSM
13	80	100.0	375	1	ATRB
14	80	100.0	375	1	ATRTC
15	80	100.0	375	1	A48324
16	80	100.0	375	1	ATCHB
17	80	100.0	375	1	ATHUB
18	80	100.0	375	1	ATHUG
19	80	100.0	375	1	ATWSB
20	80	100.0	375	1	ATMSG
21	80	100.0	375	1	ATRBB
22	80	100.0	375	1	S11222
23	80	100.0	375	2	S33386
24	80	100.0	375	2	T25272
25	80	100.0	375	2	S71125
26	80	100.0	375	2	S71124
27	80	100.0	375	2	S71126
28	80	100.0	375	2	A55001
29	80	100.0	375	2	A54728

actin - Phaffia rh
actin 7 - fruit fl
actin gamma, cytos
actin gamma, smoot
actin 8 - fruit fl
actin CyI - sea ur
Actin-1A - nematod
actin 87E - fruit
actin - fruit fly
actin, cytosolic -
actin, muscle - et
actin 15A - sea ur
actin - sea urchin
actin gamma, enter
actin - Hydra atte
actin (clone gen3)

ALIGNMENTS

RESULT 1

C43616
actin beta, cytosolic - chicken (fragment)
C:Species: Gallus gallus (chicken)
C>Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
C:Accession: C43616
R:Paterson, B.M.; Eldridge, J.D.
Science 224, 1436-1438, 1984
A:Title: Alpha-Cardiac actin is the major sarcomeric isoform expressed in embryonic avia
A:Reference number: A43616; MUID:84223949; PMID:6729461
A:Accession: C43616
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-86 <PAT>
A:Cross-references: UNIPROT:Q90736; GB:K02173; NID:g211054; PIDN:AAA98513.1; PID:g211055
C:Superfamily: actin
C:Keywords: cytosol; methylated amino acid
F:73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 80; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHOGVMV 15
Db 31 FPSIVGRPRHOGVMV 45

RESULT 2

A28258
actin 5C - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C:Accession: A28258
R:Vigoreaux, J.O.; Tobin, S.L.
Genes Dev. 1, 1161-1171, 1987
A:Title: Stage-specific selection of alternative transcriptional initiation sites from t
A:Reference number: A28258; MUID:88112795; PMID:3123314
A:Accession: A28258
A:Molecule type: mRNA
A:Residues: 1-137 <VIG>
A:Cross-references: UNIPROT:P10987
A>Note: the authors translated the codon GAG for residue 96 as Gly

C:Genetics:
A:Gene: FlyBase:Act5C
A:Cross-references: FlyBase:FBgn0000042
C:Superfamily: actin
C:Keywords: methylated amino acid
F:74/Modified site: 3'-methylhistidine (His) #status predicted
Query Match 100.0%; Score 80; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHQGVV 15
 |||||
 Db 32 FPSIVGRPRHQGVV 46

RESULT 3
 I49465
 A:Title: alpha-cardiac actin - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C:Accession: I49465; I49466
 R:Garner, I.; Minty, A.J.; Alonso, S.; Barton, P.J.R.; Buckingham, M.E.
 EMBO J. 5, 2559-2567, 1986
 A:Title: A 5' duplication of the alpha-cardiac actin gene in BALB/c mice is associated with a 1.4 kb deletion
 A:Reference number: I49465; MUID:87053822; PMID:3023046
 A:Accession: I49465
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-158 <RES>
 A:Cross-references: UNIPROT:Q61273; GB:M26775; NID:g191646; PIDN:AAA37165.1; PID:g553858
 A:Accession: I49466
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 8-158 <RES>
 A:Cross-references: GB:M26776; NID:g191649; PIDN:AAA37166.1; PID:g553859
 A:Experimental source: adult cardiac muscle, BALB/c mice
 C:Genetics:
 A:Introns: 50/3
 C:Superfamily: actin
 C:Keywords: cardiac muscle; heart

Query Match 100.0%; Score 80; DB 2; Length 158;
 Best Local Similarity 100.0%; Pred. No. 1.4e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHQGVV 15
 |||||
 Db 40 FPSIVGRPRHQGVV 54

RESULT 4
 A61043
 actin CA15 - sea squirt (Styela clava) (fragments)
 C:Species: Styela clava
 C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C:Accession: A61043
 R:Beach, R.L.; Jeffery, W.R.
 Dev. Genet. 11, 2-14, 1990
 A:Title: Temporal and spatial expression of a cytoskeletal actin gene in the ascidian Styela clava
 A:Reference number: A61043; MUID:90298580; PMID:2361333
 A:Accession: A61043
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-213 <BEA>
 A:Cross-references: UNIPROT:Q7M3Y7
 C:Comment: This sequence is expressed in cells undergoing rapid cell division.
 C:Superfamily: actin
 C:Keywords: cytoskeleton; methylated amino acid; mitosis; structural protein
 F:73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 80; DB 2; Length 213;
 Best Local Similarity 100.0%; Pred. No. 1.9e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHQGVV 15
 |||||
 Db 31 FPSIVGRPRHQGVV 45

RESULT 5
 A03000

actin 3 - fruit fly (Drosophila melanogaster) (fragments)
 C:Species: Drosophila melanogaster
 C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
 C:Accession: A03000
 R:Fyrberg, E.A.; Bond, B.J.; Hershey, N.D.; Mixter, K.S.; Davidson, N.
 Cell 24, 107-116, 1981
 A:Title: The actin genes of Drosophila: protein coding regions are highly conserved but :
 A:Reference number: A03000; MUID:81210174; PMID:6263481
 A:Accession: A03000
 A:Molecule type: DNA
 A:Residues: 1-308 <FYR>
 A:Cross-references: UNIPROT:P02572
 A:Note: there are 68 unsequenced residues between positions 160 and 161. Partial sequence
 C:Note: the authors translated the codon GTT for residue 263 as Ile
 C:Genetics:
 A:Gene: FlyBase:Act42A
 A:Cross-references: FlyBase:FBgn0000043
 A:Map position: 42A
 C:Superfamily: actin
 C:Keywords: methylated amino acid
 F:74/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 80; DB 2; Length 308;
 Best Local Similarity 100.0%; Pred. No. 2.8e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHQGVV 15
 |||||
 Db 32 FPSIVGRPRHQGVV 46

RESULT 6
 S05430
 actin beta - grass carp
 C:Species: Ctenopharyngodon idella (grass carp)
 C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
 C:Accession: S05430
 R:Liu, Z.; Zhu, Z.; Roberg, K.; Faras, A.J.; Guise, K.S.; Kapuscinski, A.R.; Hackett, P.
 Nucleic Acids Res. 17, 5850, 1989
 A:Title: The beta-actin gene of carp (Ctenopharyngodon idella).
 A:Reference number: S05430; MUID:89345185; PMID:2762162
 A:Accession: S05430
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-328 <LIU>
 A:Cross-references: UNIPROT:P83751; EMBL:M25013
 C:Genetics:
 A:Introns: 41/3; 121/3; 268/1
 C:Superfamily: actin
 C:Keywords: cytoskeleton; methylated amino acid
 F:73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 80; DB 2; Length 328;
 Best Local Similarity 100.0%; Pred. No. 3e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHQGVV 15
 |||||
 Db 31 FPSIVGRPRHQGVV 45

RESULT 7
 B25819
 actin, fetal skeletal/adult cardiac muscle - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 09-Jul-2004
 C:Accession: B25819
 R:Alonso, S.; Minty, A.; Bourlet, Y.; Buckingham, M.
 J. Mol. Evol. 23, 11-22, 1986
 A:Title: Comparison of three actin-coding sequences in the mouse: evolutionary relations
 A:Reference number: A25819; MUID:86200234; PMID:3084797
 A:Accession: B25819
 A:Molecule type: mRNA

A:Residues: 1-349 <ALO>
A:Cross-references: UNIPROT:Q61275; GB:X03767; GB:J00381; GB:M10652; NID:G49869; PIDN:CA
C:Superfamily: actin
C:Keywords: cardiac muscle; heart; methylated amino acid; muscle; skeletal muscle
F:47/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 80; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPSIVGRPRHQGMV 15
|||||
Db 5 FPSIVGRPRHQGMV 19
|||||

RESULT 8
A26559
actin type 5, cytosolic - chicken
C:Species: Gallus gallus (chicken)
C:Date: 09-Sep-1987 #sequence_revision 09-Sep-1987 #text_change 05-Dec-1997
C:Accession: A26559
R:Bergsma, D.J.; Chang, K.S.; Schwartz, R.J.
Mol. Cell. Biol. 5, 1151-1162, 1985
A:Reference number: A26559; MUID:85213487; PMID:4000121
A:Accession: A26559
A:Molecule type: DNA
A:Residues: 1-362 <BER>
C:Superfamily: actin
C:Keywords: cytosol; methylated amino acid
F:74/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 80; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPSIVGRPRHQGMV 15
|||||
Db 32 FPSIVGRPRHQGMV 46
|||||

RESULT 9
A2608
actin beta - bovine (tentative sequence)
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: E14185; A39105; A02999; A14185
R:Vandekerckhove, J.; Weber, K.
Eur. J. Biochem. 90, 451-462, 1978
A:Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain
A:Reference number: A14185; MUID:79045349; PMID:213279
A:Accession: E14185
A:Molecule type: protein
A:Residues: 1-374 <VAN>
A:Cross-references: UNIPROT:P60712
A:Note: only peptides that differed in composition from the corresponding peptides of ra
R:Degen, J.L.; Neubauer, M.G.; Degen, S.J.F.; Seyfried, C.E.; Morris, D.R.
J. Biol. Chem. 258, 12153-12162, 1983
A:Title: Regulation of protein synthesis in mitogen-activated bovine lymphocytes. Analy
A:Reference number: A39105; MUID:84032385; PMID:6195151
A:Accession: A39105
A:Molecule type: mRNA
A:Residues: 76-227;344-374 <DEG>
A:Cross-references: GB:K00622; GB:K00623
A:Note: actins beta and gamma were not distinguished in this study
C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
C:Superfamily: actin
C:Keywords: blocked amino end; cell motility; cytoskeleton; methylated amino acid; micro
F:1/Modified site: blocked amino end (Asp) (probably acetylated) #status experimental
F:72/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 80; DB 1; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPSIVGRPRHQGMV 15
|||||
Db 30 FPSIVGRPRHQGMV 44
|||||

RESULT 10
A2608
actin gamma - bovine (tentative sequence)
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: B14185; A02999
R:Vandekerckhove, J.; Weber, K.
Eur. J. Biochem. 90, 451-462, 1978
A:Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain
A:Reference number: A14185; MUID:79045349; PMID:213279
A:Accession: B14185
A:Molecule type: protein
A:Residues: 1-374 <VAN>
A:Cross-references: UNIPROT:P02571
A:Note: only peptides that differed in composition from the corresponding peptides of ra
C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
C:Superfamily: actin
C:Keywords: blocked amino end; cell motility; cytoskeleton; methylated amino acid; micro
F:1/Modified site: blocked amino end (Glu) (probably acetylated) #status experimental
F:72/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 80; DB 1; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPSIVGRPRHQGMV 15
|||||
Db 30 FPSIVGRPRHQGMV 44
|||||

RESULT 11
JC5818
gamma-actin - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C:Accession: JC5818; PC4501
R:Hauschildt, S.; Schwarz, C.; Heine, H.; Ulmer, A.J.; Flad, H.D.; Rietschel, E.T.; Jens
Biochem. Biophys. Res. Commun. 241, 670-674, 1997
A:Title: Actin: A target of lipopolysaccharide-induced phosphorylation in human monocytes
A:Reference number: JC5818; MUID:98096379; PMID:9434766
A:Accession: JC5818
A:Molecule type: protein
A:Residues: 1-374 <HAU>
A:Cross-references: UNIPROT:P02571
A:Experimental source: monocyte
A:Accession: PC4501
A:Molecule type: protein
A:Residues: 1-61;84-112;147-190;196-209;215-253;335-358 <HA2>
A:Experimental source: monocyte
C:Comment: This protein is involved in a signal transduction that eventually leads to mo
C:Superfamily: actin

Query Match 100.0%; Score 80; DB 2; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPSIVGRPRHQGMV 15
|||||
Db 30 FPSIVGRPRHQGMV 44
|||||

RESULT 12
A2608
actin, aortic smooth muscle - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 06-Sep-1996
C:Accession: A02997; S13480

R;Vandekerckhove, J.; Weber, K.
Differentiation 14, 123-133, 1979
A;Title: The complete amino acid sequence of actins from bovine aorta, bovine heart, bovine thymus.
A;Reference number: A02997; MUID:80047657; PMID:499690
A;Accession: A02997
A;Molecule type: protein
A;Residues: 1-375 <VAN>
R;Zevgolis, V.G.; Sotiropoulos, T.G.; Evangelopoulos, A.E.
Biochim. Biophys. Acta 1091, 222-230, 1991
A;Title: Phosphorylase kinase from bovine stomach smooth muscle: a Ca(2+)-dependent protein.
A;Reference number: S13480; MUID:91137633; PMID:1995080
A;Accession: S13480
A;Molecule type: protein
A;Residues: 40-49 <ZEV>
A;Experimental source: stomach
A;Note: This material appears to be actin of aortic smooth muscle type or a related molecule.
C;Superfamily: actin
C;Keywords: acetylated amino end; methylated amino acid; muscle contraction
F;1/Modified site: acetylated amino end (Glu) #status predicted
F;73/Modified site: 3'-methylhistidine (His) #status experimental

Query Match 100.0%; Score 80; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHQGVWV 15
| | | | | | | | | | | | | | | | | | | | | |
Db 31 FPSIVGRPRHQGVWV 45

RESULT 13
ATRB
actin, skeletal muscle - rabbit
N;Alternate names: F-actin
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text change 07-May-1999
C;Accession: A92182; A14185; S65873; S70610; S44393; A02994
R;Collins, J.H.; Elzinga, M.
J. Biol. Chem. 250, 5915-5920, 1975
A;Title: The primary structure of actin from rabbit skeletal muscle. Completion and analysis.
A;Reference number: A92182; MUID:75211334; PMID:1150665
A;Accession: A92182
A;Molecule type: protein
A;Residues: 1-2, 1, 4, D, 6-11, D, 13-73, W, 74-78, 80-234, 236-308, T, 310-375 <COL>
A;Note: This is the final paper in a series
A;Note: This sequence has been revised in references A14185 and A90406
R;Vandekerckhove, J.; Weber, K.
Eur. J. Biochem. 90, 451-462, 1978
A;Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain and rabbit skeletal muscle.
A;Reference number: A14185; MUID:79045349; PMID:213279
A;Accession: A14185
A;Molecule type: protein
A;Residues: 1-18;69-84 <VAN>
R;Lu, R.C.; Elzinga, M.
Biochemistry 16, 5801-5806, 1977
A;Title: Partial amino acid sequence of brain actin and its homology with muscle actin.
A;Reference number: A90406; MUID:78060866; PMID:588555
A;Contents: annotation
A;Note: residue 235 has been added and residue 309 has been revised
R;Vandat, A.; Miller, C.; Phillips, M.; Muhltad, A.; Reisler, E.
FEBS Lett. 365, 149-151, 1995
A;Title: A novel 27/16 kDa form of subunit cleaved actin: structural and functional characterization.
A;Reference number: S65873; MUID:95300963; PMID:7781768
A;Accession: S65873
A;Molecule type: protein
A;Residues: 235-241 <VAN>
R;Strzelecka-Golaszewska, H.; Wozniak, A.; Hult, T.; Lindberg, U.
Biochem. J. 316, 713-721, 1996
A;Title: Effects of the type of divalent cation, Ca2+ or Mg2+, bound at the high-affinity site on the actin monomer.
A;Reference number: S70610; MUID:96265033; PMID:8670143
A;Accession: S70610
A;Molecule type: protein

A;Residues: 48-54;68-72;235-243 <STR>
A;Experimental source: skeletal muscle
R;Bertrand, R.; Derancourt, J.; Kassab, R.
FEBS Lett. 345, 113-119, 1994
A;Title: The covalent maleimidebenzoyl-actin-myosin head complex. Cross-linking of the 5' and 3' ends of actin.
A;Reference number: S44393; MUID:94259162; PMID:8200441
A;Accession: S44393
A;Molecule type: protein
A;Residues: 48-64 <BER>
A;Experimental source: skeletal muscle
C;Superfamily: actin
C;Keywords: acetylated amino end; ATP binding; methylated amino acid; muscle contraction
F;1-375/Product: actin #status experimental <MAT>
F;1/Modified site: acetylated amino end (Asp) #status experimental
F;73/Modified site: 3'-methylhistidine (His) #status experimental

Query Match 100.0%; Score 80; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHQGVWV 15
| | | | | | | | | | | | | | | | | | | | | |
Db 31 FPSIVGRPRHQGVWV 45

RESULT 14
ATRIC
actin beta - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jun-1983 #sequence revision 13-Jun-1983 #text change 22-Jun-1999
C;Accession: A38571; A02999
R;Nudel, U.; Zakut, R.; Shani, M.; Neuman, S.; Levy, Z.; Yaffe, D.
Nucleic Acids Res. 11, 1759-1771, 1983
A;Title: The nucleotide sequence of the rat cytoplasmic beta-actin gene.
A;Reference number: A38571; MUID:83168920; PMID:6300777
A;Accession: A38571
A;Molecule type: DNA
A;Residues: 1-375 <NUD>
A;Cross-references: GB:J00691; NID:q202653; PIDN:AAA40657.1; PID:q202654
C;Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins, alpha-actinin and beta-actinin.
C;Genetics:
A;Introns: 41/3; 121/3; 268/1; 328/3
C;Superfamily: actin
C;Keywords: cell motility; cytoskeleton; methylated amino acid; microfilament; mitosis; F-actin
F;2-375/Product: actin beta #status predicted <MAT>
F;73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 80; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHQGVWV 15
| | | | | | | | | | | | | | | | | | | | | |
Db 31 FPSIVGRPRHQGVWV 45

RESULT 15
A48324
actin beta, cytoskeletal - common carp
C;Species: Cyprinus carpio (common carp)
C;Date: 03-Feb-1994 #sequence revision 11-Apr-1997 #text change 09-Jul-2004
C;Accession: A48324
R;Liu, Z.; Zhu, Z.; Roberg, K.; Faras, A.; Guise, K.; Kapuscinski, A.R.; Hackett, P.B.
DNA Seq. 1, 125-136, 1990
A;Title: Isolation and characterization of beta-actin gene of carp (Cyprinus carpio).
A;Reference number: A48324; MUID:92190540; PMID:2134183
A;Accession: A48324
A;Molecule type: DNA
A;Residues: 1-375 <LIU>
A;Cross-references: UNIPROT:P83750; GB:M24113; NID:g213041; PIDN:AAA68896.1; PID:g213042
A;Note: The authors translated the codon TTC for residue 21 as Pro, AAG for residue 50 as Pro
A;Note: the authors failed to translated the codon GGT for residue 42 as Gly

C;Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
C;Genetics:
A;Introns: 41/3; 121/3; 268/3; 328/3
C;Superfamily: actin
C;Keywords: acetylated amino end; cell motility; cytoskeleton; methylated amino acid; mi
F;2-375/Product: actin beta, cytoskeletal #status predicted <MAT>-
F;2/Modified site: acetylated amino end (Asp) (in mature form) #status predicted
F;73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 80; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHOGVMV 15
|||
Db 31 FPSIVGRPRHOGVMV 45
|||

Search completed: April 8, 2005, 10:53:04
Job time : 9.33333 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 57.8667 seconds
(without alignments)
132.739 Million cell updates/sec

Title: US-09-423-351C-2
Perfect score: 80
Sequence: 1 FPSIVGRPRHQGMV 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	80	100.0	26	Q6Q298	Q6Q298 oviz aries
2	80	100.0	53	Q6AW41	Q6AW41 bombyx mori
3	80	100.0	78	Q61375	Q61375 schmidtea p
4	80	100.0	78	Q61376	Q61376 schmidtea p
5	80	100.0	78	Q61377	Q61377 schmidtea p
6	80	100.0	79	Q95183	Q95183 oryctolagus
7	80	100.0	86	Q90736	Q90736 gallus gall
8	80	100.0	91	Q72211	Q72211 salvelinus
9	80	100.0	92	Q86CVA	Q86CVA drosophila
10	80	100.0	96	Q86FV7	Q86FV7 drosophila
11	80	100.0	99	Q9QZB4	Q9QZB4 cavia porce
12	80	100.0	104	Q86SB7	Q86SB7 gryllus bim
13	80	100.0	108	Q18548	Q18548 lytechinus
14	80	100.0	108	Q18550	Q18550 lytechinus
15	80	100.0	121	Q83G71	Q83G71 oreochromis
16	80	100.0	121	Q78CQ1	Q78CQ1 pseudopleur
17	80	100.0	129	Q6VBE4	Q6VBE4 locusta mig
18	80	100.0	130	Q93298	Q93298 pseudopleur
19	80	100.0	139	Q9DFK2	Q9DFK2 gillithyrs
20	80	100.0	144	Q90YX9	Q90YX9 fundulus he
21	80	100.0	150	Q804Y9	Q804Y9 ictalurus p
22	80	100.0	151	Q61274	Q61274 mus musculu
23	80	100.0	151	Q9PSV5	Q9PSV5 oryzias lat
24	80	100.0	158	Q61273	Q61273 mus musculu
25	80	100.0	164	1 ACT SPOLI	Q11212 spodoptera
26	80	100.0	165	Q17477	Q17477 haliothis ru
27	80	100.0	184	Q11209	Q11209 canis fami
28	80	100.0	186	Q8X190	Q8X190 paxillus in
29	80	100.0	189	Q8SPX4	Q8SPX4 canis fami
30	80	100.0	191	Q64G12	Q64G12 oxyuranus s
31	80	100.0	198	Q6Y250	Q6Y250 pagrus majo

32	80	100.0	202	Q810R5	Q810R5 mus musculu
33	80	100.0	212	Q6ZYL2	Q6ZYL2 arion lusit
34	80	100.0	213	Q7M3V7	Q7M3V7 styela clav
35	80	100.0	225	Q64G13	Q64G13 oxyuranus s
36	80	100.0	235	Q7XB23	Q7XB23 lotharella
37	80	100.0	235	Q7XB24	Q7XB24 lotharella
38	80	100.0	235	Q7XB25	Q7XB25 lotharella
39	80	100.0	236	Q6RXX3	Q6RXX3 penaeus van
40	80	100.0	237	Q7XB21	Q7XB21 lotharella
41	80	100.0	237	Q7XB22	Q7XB22 lotharella
42	80	100.0	238	Q7XB20	Q7XB20 lotharella
43	80	100.0	239	Q7XB28	Q7XB28 chlorarachn
44	80	100.0	254	Q7Z7J6	Q7Z7J6 homo sapien
45	80	100.0	273	Q7Q7K4	Q7Q7K4 anopheles g

ALIGNMENTS

RESULT 1

Q6Q298	PRELIMINARY;	PRT;	26 AA.
AC	Q6Q298;		
DT	05-JUL-2004 (Tremblrel. 27, Created)		
DT	05-JUL-2004 (Tremblrel. 27, Last sequence update)		
DT	05-JUL-2004 (Tremblrel. 27, Last annotation update)		
DE	Beta actin (Fragment).		
OS	Ovis aries (Sheep).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC	Caprinae; Ovis.		
OX	NCBI_TaxID=9940;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Abomasum;		
RA	Shanmuganathan T., Hickford J.G.H., Savill M., Sykes A.R.;		
RL	Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY566300; AAS68014.1; -		
FT	NON_TER 1		
FT	NON_TER 26		
SQ	SEQUENCE 26 AA; 2802 MW; C75DA20C92E36C4B CRC64;		

Query Match 100.0%; Score 80; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 FPSIVGRPRHQGMV 15
Db	2 FPSIVGRPRHQGMV 16

RESULT 2

Q6AW41	PRELIMINARY;	PRT;	53 AA.
ID	Q6AW41		
AC	Q6AW41;		
DT	25-OCT-2004 (Tremblrel. 28, Created)		
DT	25-OCT-2004 (Tremblrel. 28, Last sequence update)		
DT	25-OCT-2004 (Tremblrel. 28, Last annotation update)		
DE	Cytoplasmic actin (Fragment).		
OS	Bombyx mori (Silk moth).		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Lepidoptera; Glossata; Ditryaia; Bombycoidea;		
OC	Bombycidae; Bombyx.		
OX	NCBI_TaxID=7091;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Daizo; TISSUE=Silk gland;		
RA	Shiomi K., Kajimura Z., Nakagaki M., Yamashita O.;		
RT	"Baculovirus-mediated efficient gene transfer into the central nervous		
RL	system of the silkworm, Bombyx mori.";		
RL	Nihon Sanehigaku Zasshi 72:149-155 (2003).		
RN	[2]		
RP	SEQUENCE FROM N.A.		

```

RC STRAIN=Daizo; TISSUE=Silk gland;
RA Shomi K.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
RM EMBL; AB186491; BAD35130.1; -.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON TER 53
SQ SEQUENCE 53 AA; 5465 MW; 227AA8B4872EBA86 CRC64;

Query Match 100.0%; Score 80; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHQGVV 15
Db 32 FPSIVGRPRHQGVV 46

RESULT 3
O61375 PRELIMINARY; PRT; 78 AA.
ID O61375
AC O61375;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Actin 1 (Fragment).
GN Name=DpAct1;
OS Schmidtea polychoa.
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC Paludicola; Dugesidae; Schmidtea.
OX NCBI_TaxID=50054;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98186847; PubMed=9518500; DOI=10.1093/nar/26.8.2031;
RA Fagotti A., Gabbiani G., Pascolini R., Neuville P.;
RT "Multiple isoform recovery (MIR)-PCR: a simple method for the
isolation of related mRNA isoforms.";
RL Nucleic Acids Res. 26:2031-2033(1998).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
in various types of cell motility and are ubiquitously expressed
in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AF027161; AAC38981.1; -.
DR HSSP; P02577; INMI.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
KW Structural protein.
FT NON TER 78
SQ SEQUENCE 78 AA; 8205 MW; 572BAB2698C24404 CRC64;

Query Match 100.0%; Score 80; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHQGVV 15
Db 32 FPSIVGRPRHQGVV 46

RESULT 4
O61376 PRELIMINARY; PRT; 78 AA.
ID O61376
AC O61376;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Actin 2 (Fragment).

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GN Name=DpAct2;
OS Schmidtea polychoa.
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC Paludicola; Dugesidae; Schmidtea.
OX NCBI_TaxID=50054;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98186847; PubMed=9518500; DOI=10.1093/nar/26.8.2031;
RA Fagotti A., Gabbiani G., Pascolini R., Neuville P.;
RT "Multiple isoform recovery (MIR)-PCR: a simple method for the
isolation of related mRNA isoforms.";
RL Nucleic Acids Res. 26:2031-2033(1998).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
in various types of cell motility and are ubiquitously expressed
in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AF027162; AAC38982.1; -.
DR HSSP; P02577; INMI.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
KW Structural protein.
FT NON TER 78
SQ SEQUENCE 78 AA; 8255 MW; B9DFF9B28E4ADB0E CRC64;

Query Match 100.0%; Score 80; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHQGVV 15
Db 32 FPSIVGRPRHQGVV 46

RESULT 5
O61377 PRELIMINARY; PRT; 78 AA.
ID O61377
AC O61377;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Actin 3 (Fragment).
GN Name=DpAct3;
OS Schmidtea polychoa.
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC Paludicola; Dugesidae; Schmidtea.
OX NCBI_TaxID=50054;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98186847; PubMed=9518500; DOI=10.1093/nar/26.8.2031;
RA Fagotti A., Gabbiani G., Pascolini R., Neuville P.;
RT "Multiple isoform recovery (MIR)-PCR: a simple method for the
isolation of related mRNA isoforms.";
RL Nucleic Acids Res. 26:2031-2033(1998).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
in various types of cell motility and are ubiquitously expressed
in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AF027163; AAC38983.1; -.
DR HSSP; P02577; INMI.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.

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KW Structural protein. 78
FT NON TER 78
SQ SEQUENCE 78 AA; 8299 MW; B9DF1108E4ADBOE CRC64;

Query Match 100.0%; Score 80; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPSIVGRPRHQGVV 15
DB 32 FPSIVGRPRHQGVV 46

RESULT 6
Q95L83
ID Q95L83 PRELIMINARY; PRT; 79 AA.
AC Q95L83
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta-actin (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22306422; PubMed=12388084;
RA Wang D.-A., Du H., Jagger J.H., Brindley D.N., Tigyi G.J.,
RA Watsky M.A.;
RT "Injury-elicited differential transcriptional regulation of
RT phospholipid growth factor receptors in the cornea.";
RL Am. J. Physiol. Cell Physiol. 283:C1646-C1654(2002).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AF04278; AAL01885.1; -.
DR HSSP; P02577; 1NM1.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
KW Structural protein.
FT NON TER 1
FT NON TER 79
SQ SEQUENCE 79 AA; 8420 MW; 05056E4E2AC092F8 CRC64;

Query Match 100.0%; Score 80; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPSIVGRPRHQGVV 15
DB 33 FPSIVGRPRHQGVV 47

RESULT 7
Q90736
ID Q90736 PRELIMINARY; PRT; 86 AA.
AC Q90736
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta-actin (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.

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OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84223949; PubMed=6729461;
RA Paterson B.M., Eldridge J.D.;
RT "alpha-Cardiac actin is the major sarcomeric isoform expressed in
RT embryonic avian skeletal muscle.";
RL Science 224:1436-1438(1984).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; K02173; AAA98513.1; -.
DR PIR; C43616; C43616.
DR HSSP; P02577; 1NM1.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
KW Structural protein.
FT NON TER 86
FT NON TER 86
SQ SEQUENCE 86 AA; 9351 MW; A55285196A328B6E CRC64;

Query Match 100.0%; Score 80; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPSIVGRPRHQGVV 15
DB 31 FPSIVGRPRHQGVV 45

RESULT 8
Q7Z211
ID Q7Z211 PRELIMINARY; PRT; 91 AA.
AC Q7Z211
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-actin (Fragment).
OS Salvelinus alpinus (Arctic char).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX NCBI_TaxID=8036;
RN [1]
RP SEQUENCE FROM N.A.
RA McGowan C., Davidson E.A., Davidson W.S.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AY262761; AAP31127.1; -.
DR HSSP; P02577; 1NM1.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
KW Structural protein.
FT NON TER 91
FT NON TER 91
SQ SEQUENCE 91 AA; 10063 MW; 7118DB66663CD895C CRC64;

Query Match 100.0%; Score 80; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
Qy 1 FPSIVGRPRHQGMV 15
Db 29 FPSIVGRPRHQGMV 43

RESULT 9
Q86CV4 PRELIMINARY; PRT; 96 AA.
AC Q86CV4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Actin E2 (Fragment)
GN Name=ActE2;
OS Drosophila novamexicana.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=47314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=15010-1031.0;
EX MEDLINE=22480340; PubMed=12574518; DOI=10.1073/pnas.0336368100;
RA Wittkopp P.J., Williams B.L., Selegue J.E., Carroll S.B.;
RT "Drosophila pigmentation evolution: divergent genotypes underlying
convergent phenotypes.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:1808-1813(2003).
CC -|- FUNCTION: Actins are highly conserved proteins that are involved
in various types of cell motility and are ubiquitously expressed
in all eukaryotic cells (By similarity).
CC -|- SIMILARITY: Belongs to the actin family.
DR EMBL; AY165541; AAP21565.1; -.
DR HSSP; P02568; ILCU.
DR FlyBase; FBgn0066281; Dame\ActE2.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
KW Structural protein.
FT NON_TER 96
SQ SEQUENCE 96 AA; 10610 MW; 1454B7D9DD3F3564 CRC64;

Query Match 100.0%; Score 80; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHQGMV 15
Db 32 FPSIVGRPRHQGMV 46

RESULT 11
Q9QZB4 PRELIMINARY; PRT; 99 AA.
AC Q9QZB4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytoplasmic actin (Fragment).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal gland;
RA Buelow H.E., Bernhardt R.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -|- FUNCTION: Actins are highly conserved proteins that are involved
in various types of cell motility and are ubiquitously expressed
in all eukaryotic cells (By similarity).
CC -|- SIMILARITY: Belongs to the actin family.
DR EMBL; AF191277; AAF13923.1; -.
DR HSSP; P02577; INM1.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
KW Structural protein.
FT NON_TER 99
SQ SEQUENCE 99 AA; 10973 MW; 0562B645B8DAF17B CRC64;

Query Match 100.0%; Score 80; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHQGMV 15
Db 32 FPSIVGRPRHQGMV 46

RESULT 10
Q86FV7 PRELIMINARY; PRT; 96 AA.
AC Q86FV7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Actin E2 (Fragment)
GN Name=ActE2;
OS Drosophila americana (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=40366;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=15010-0951.0;
```



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aps 0;
```

Fri Apr 8 14:14:25 2005

Qy 1 FPSIVGRPRHQGMV 15
 |||||
 Db 18 FPSIVGRPRHQGMV 32

RESULT 15

Q8JG71 PRELIMINARY; PRT; 121 AA.
 AC Q8JG71;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Beta-actin (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidae;
 OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22414672; PubMed=12527420; DOI=10.1016/S0167-4781(02)00534-1;
 RA Hwang G.-L., Rahman M.A., Razak S.A., Schm F., Farahmand H., Smith A.,
 RA Brooks C., Maclean N.;
 RT "Isolation and characterization of tilapia beta-actin promoter and
 comparison of its activity with carp beta-actin promoter.";
 RL Biochim. Biophys. Acta 1625:11-18(2003).
 CC -!- FUNCTION: Actins are highly conserved proteins that are involved
 in various types of cell motility and are ubiquitously expressed
 in all eukaryotic cells (By similarity).
 CC -!- SIMILARITY: Belongs to the actin family.
 DR EMBL; AY116536; AAM66751.1; -.
 DR HSP; P10983; ID4X.
 DR GO; GO:0005884; C:actin filament; IEA.
 DR GO; GO:0003774; F:motor activity; IEA.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
 DR InterPro; IPR004001; Actin.
 DR InterPro; IPR004000; Actin_like.
 DR Pfam; PF00022; Actin; 1.
 DR PRINTS; PRO0190; ACTIN.
 DR PROSITE; PS00406; ACTINS 1; 1.
 DR PROSITE; PS01132; ACTINE_ACT_LIKE; 1.
 KW Structural protein.
 FT NON_TER 121 121
 SQ SEQUENCE 121 AA; 13458 MW; 04A58F271BBA0898 CRC64;

Query Match 100.0%; Score 80; DB 2; Length 121;
 Best Local Similarity 100.0%; Pred. No. 4.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPSIVGRPRHQGMV 15
 |||||
 Db 31 FPSIVGRPRHQGMV 45

Search completed: April 8, 2005, 12:03:06
 Job time : 59.8667 secs

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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 62.4 Seconds
(without alignments)
92.971 Million cell updates/sec

Title: US-09-423-351C-3

Perfect score: 82

Sequence: 1 GRPRHQGVWVGQK 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	82	100.0	15	2	Aaw92529 Beta-acti
2	82	100.0	19	2	Aaw92543 Beta-acti
3	82	100.0	105	5	Abp42469 Human ova
4	82	100.0	157	4	Abb66853 Drosophil
5	82	100.0	201	5	Abp43176 Human ova
6	82	100.0	204	5	Abp43016 Human ova
7	82	100.0	310	8	Adr38362 piGA3Cy3G
8	82	100.0	342	7	Adm05323 Human pro
9	82	100.0	374	3	Abb12985 Human bet
10	82	100.0	375	1	Aap61532 Sequence
11	82	100.0	375	2	Aar50328 Drug resi
12	82	100.0	375	3	Aab15017 Posttrans
13	82	100.0	375	3	Aay94569 Human car
14	82	100.0	375	3	Aab15016 Posttrans
15	82	100.0	375	5	Abb77395 Human act
16	82	100.0	375	6	Abm64271 Angiogene
17	82	100.0	375	6	Abm04830 Rat cytop
18	82	100.0	375	7	Abm85212 Rat actin
19	82	100.0	375	7	Ades61174 Rat prote
20	82	100.0	375	7	Adf30525 Rat angio
21	82	100.0	375	7	Adi63062 Human apo
22	82	100.0	375	7	Adi62970 Human apo
23	82	100.0	375	7	Adi63040 Human apo
24	82	100.0	375	8	Adi13002 Human ste
25	82	100.0	375	8	Adj78489 Actin pro

26	82	100.0	375	8	ADL14103	Adl14103 Human ear
27	82	100.0	375	8	ADP04899	Adp04899 Sea squir
28	82	100.0	375	8	ADP12391	Adp12391 Protein e
29	82	100.0	375	8	ADQ26098	Adq26098 Gamma 1 a
30	82	100.0	375	8	ASO84772	Aso84772 Human can
31	82	100.0	375	8	ABM80841	Abm80841 Tumour-as
32	82	100.0	375	8	ADN23274	Adn23274 Bacterial
33	82	100.0	375	8	ADS88828	Ads88828 Amino aci
34	82	100.0	375	8	ADS88825	Ads88825 Amino aci
35	82	100.0	375	8	ADS88826	Ads88826 Amino aci
36	82	100.0	375	8	ADS88827	Ads88827 Amino aci
37	82	100.0	376	2	AAW19799	Aaw19799 Gamma-smo
38	82	100.0	376	4	ABB61322	Abb61322 Drosophil
39	82	100.0	376	4	ABB61322	Abb61322 Drosophil
40	82	100.0	376	4	ABB60354	Abb60354 Drosophil
41	82	100.0	376	4	ABB64853	Abb64853 Drosophil
42	82	100.0	376	4	ABB63315	Abb63315 Drosophil
43	82	100.0	376	6	ABR62327	AbR62327 Pacific w
44	82	100.0	376	8	ADN03845	Adn03845 Antipsoi
45	82	100.0	377	3	AAB15014	Aab15014 Human ear

ALIGNMENTS

RESULT 1

AAW92529

ID AAW92529 standard; peptide; 15 AA.

XX AC AAW92529;

XX AC AAW92529;

DT 26-APR-1999 (first entry)

XX DE Beta-actin reference peptide substrate #3.

XX DE Beta-actin reference peptide substrate #3.

Peptide substrate; CCT; eukaryotic type II chaperonin complex; cyclin; binding agent; substrate-binding site; SBS; substrate folding; actin; tubulin; treatment; cancer; anticancer drug; viral infection; screening; reduced toxicity.

XX OS Synthetic.

XX OS Synthetic.

XX PN WO9853322-A1.

XX PD 26-NOV-1998.

XX PF 22-MAY-1998; 98WO-GB001485.

XX PR 23-MAY-1997; 97GB-00010762.

XX PA (CANC-) INST CANCER RES ROYAL CANCER HOSPITAL.

XX PI Willison K, Hynes G, Liou AK;

XX DR WPI; 1999-070162/06.

Identifying specific binding agents for substrate binding site in CCT chaperonin complex - also new peptide binding agents and their mimetics, and peptides containing a specific CCT binding site, used for treating cancer.

XX PS Disclosure; Fig 10; 97pp; English.

This invention describes a method which uses the CCT (eukaryotic type II chaperonin) complex or part of it, for identifying a binding agent that can occupy a substrate-binding site (SBS) on the CCT complex. By binding to the CCT complex, the binding agents block an SBS so that biological activity of the CCT complex is affected, particularly its ability to fold substrates such as actin, tubulin and cyclin. The binding agents are useful for treatment of cancer, particularly when used in combination with an anticancer drug, or viral infections. Nucleic acid fragments are used to screen for agents, e.g. binding agents that modulate interaction between the CCT complex and a protein that is to be folded. The binding

CC agents may target cells that are actively synthesising tubulin etc.
 CC (unlike known microtubule-stabilising agents that affect all cells), so
 CC should have reduced toxicity for normal cells. AAW92527-W92541 are
 CC peptide substrates used in the method of the invention
 SQ Sequence 15 AA;

Query Match 100.0%; Score 82; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6.8e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRPRHOGVWVGWGQK 15
 DB 1 GRPRHOGVWVGWGQK 15

RESULT 2
 AAW92543
 ID AAW92543 standard; peptide; 19 AA.

AC AAW92543;

DT 26-APR-1999 (first entry)

DE Beta-actin array biotinylated peptide substrate #1.

XX Peptide substrate; CCT; eukaryotic type II chaperonin complex; cyclin;
 KW binding agent; substrate-binding site; SBS; substrate folding; actin;
 KW tubulin; treatment; cancer; anticancer drug; viral infection; screening;
 KW reduced toxicity.

OS Synthetic.

XX Key Location/Qualifiers
 FH Modified-site 1
 FT /note= "Ser modified by biotin"

XX WO9853322-A1.

PD 26-NOV-1998.

PF 22-MAY-1998; 98WO-GB001485.

PR 23-MAY-1997; 97GB-00010762.

XX (CANC-) INST CANCER RES ROYAL CANCER HOSPITAL.

XX Willison K, Hynes G, Liou AK;

XX WPI; 1999-070162/06.

XX Identifying specific binding agents for substrate binding site in CCT
 PT chaperonin complex - also new peptide binding agents and their mimetics,
 PT and peptides containing a specific CCT binding site, used for treating
 PT cancer.

PS Disclosure; Fig 11; 97pp; English.

XX This invention describes a method which uses the CCT (eukaryotic type II
 CC chaperonin) complex or part of it, for identifying a binding agent that
 CC can occupy a substrate-binding site (SBS) on the CCT complex. By binding
 CC to the CCT complex, the binding agents block an SBS so that biological
 CC activity of the CCT complex is affected, particularly its ability to fold
 CC substrates such as actin, tubulin and cyclin. The binding agents are
 CC useful for treatment of cancer, particularly when used in combination
 CC with an anticancer drug, or viral infections. Nucleic acid fragments are
 CC used to screen for agents, e.g. binding agents that modulate interaction
 CC between the CCT complex and a protein that is to be folded. The binding
 CC agents may target cells that are actively synthesising tubulin etc.
 CC (unlike known microtubule-stabilising agents that affect all cells), so
 CC should have reduced toxicity for normal cells. AAW92543-W92549 are
 CC peptide substrates used in the method of the invention

SQ Sequence 19 AA;

Query Match 100.0%; Score 82; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 8.7e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRPRHOGVWVGWGQK 15
 DB 5 GRPRHOGVWVGWGQK 19

RESULT 3
 ABP42469
 ID ABP42469 standard; protein; 105 AA.

AC ABP42469;

XX 22-AUG-2002 (first entry)

DE Human ovarian antigen HOCQ94, SEQ ID NO:3601.

XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive.

OS Homo sapiens.

XX WO200200677-A1.

XX 03-JAN-2002.

XX 07-JUN-2001; 2001WO-US018569.

XX 07-JUN-2000; 2000US-0209467P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Birse CE, Rosen CA;

XX WPI; 2002-147878/19.

XX N-PSDB; ABQ55546.

XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 PT cancer), immune disorders, cardiovascular disorders and neurological
 PT diseases.

PS Claim 11; SEQ ID NO 3601; 2922pp; English.

XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovary and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis), and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,

CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 105 AA;

Query Match 100.0%; Score 82; DB 5; Length 105;
 Best Local Similarity 100.0%; Pred. No. 5.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRPRHQGVVMGQK 15
 DB 37 GRPRHQGVVMGQK 51

RESULT 4
 ID ABB66853
 XX ABB66853 standard; protein; 157 AA.

AC ABB66853;

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 27351.

XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

XX 11-JUL-2000; 2000US-00614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

XX N-PSDB; ABL10956.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.

XX Disclosure; SEQ ID NO 27351; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 157 AA;

Query Match 100.0%; Score 82; DB 4; Length 157;
 Best Local Similarity 100.0%; Pred. No. 7.7e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRPRHQGVVMGQK 15
 DB 37 GRPRHQGVVMGQK 51

RESULT 5
 ID ABP43176
 XX ABP43176 standard; protein; 201 AA.

AC ABP43176;

XX 22-AUG-2002 (first entry)

XX Human ovarian antigen HVQCQ49, SEQ ID NO:4308.

XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive.

XX Homo sapiens.

XX WO200200677-A1.

XX 03-JAN-2002.

XX 07-JUN-2001; 2001WO-US018569.

XX 07-JUN-2000; 2000US-0209467P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Birse CE, Rosen CA;

XX WPI; 2002-147878/19.

XX N-PSDB; ABQ56253.

XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 PT cancer), immune disorders, cardiovascular disorders and neurological
 PT diseases.

XX Claim 11; SEQ ID NO 4308; 2922pp; English.

XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovary and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis), and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders

CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 201 AA;
 SQ
 Query Match 100.0%; Score 82; DB 5; Length 201;
 Best Local Similarity 100.0%; Pred. No. 9.9e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GRPRHQGVWVGQK 15
 Db 53 GRPRHQGVWVGQK 67
 RESULT 6
 ID ABP43016 standard; protein; 204 AA.
 AC ABP43016;
 XX
 DT 22-AUG-2002 (first entry)
 XX
 DE Human ovarian antigen HSPB24, SEQ ID NO:4148.
 DE
 KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive.
 XX
 OS Homo sapiens.
 XX
 PN WO200200677-A1.
 XX
 PD 03-JAN-2002.
 XX
 PF 07-JUN-2001; 2001WO-US018569.
 XX
 PR 07-JUN-2000; 2000US-0209467P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Birse CE, Rosen CA;
 XX
 DR WPI; 2002-147878/19.
 DR N-PSDB; ABQ56093.
 XX
 PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 PT cancer), immune disorders, cardiovascular disorders and neurological
 PT diseases.
 XX
 PS Claim 11; SEQ ID NO 4148; 2922bp; English.
 XX
 CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen

CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prophagosing or preventing various ovary and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 204 AA;
 SQ
 Query Match 100.0%; Score 82; DB 5; Length 204;
 Best Local Similarity 100.0%; Pred. No. 1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GRPRHQGVWVGQK 15
 Db 56 GRPRHQGVWVGQK 70
 RESULT 7
 ID ADR38362 standard; protein; 310 AA.
 XX ADR38362;
 AC ADR38362;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE pigA3Cy3GFP plasmid protein product (Cycle3 GFP under an actin promoter).
 XX
 KW piggyBac; transposon; transposase; gene transfer; plasmid; Cycle3 GFP;
 KW actin promoter.
 XX
 OS Bombyx mori.
 OS Synthetic.
 OS Unidentified.
 XX
 PH Key Location/Qualifiers
 FT Misc-difference 20 /note= "Encoded by GCC"
 FT
 XX JP2004236642-A.
 PN
 XX 26-AUG-2004.
 PD
 XX 10-FEB-2003; 2003JP-00032306.
 PF
 XX 10-FEB-2003; 2003JP-00032306.
 PR
 XX (TORA) TORAY IND INC.
 PA
 XX WPI; 2004-608233/59.
 DR N-PSDB; ADR38361.
 XX
 PT Introducing foreign gene into insect cell, involves introducing DNA
 PT having foreign gene integrated between inverted repeat sequences of
 PT piggyBac transposon and piggyBac transposase that acts on inverted repeat

PT sequence.
 PS Disclosure; Page; 25pp; Japanese.
 XX
 CC This invention relates to a novel method for introducing a foreign gene
 CC into an insect cell. Specifically, it refers to a foreign gene occurring
 CC between inverted repeat sequences of a piggyBac transposon and using a
 CC piggyBac transposase for gene transfer to give a high recombinant
 CC efficiency. The present invention describes the insect cell as that of
 CC Lepidoptera insect origin, preferably it is the silk worm Bombyx mori,
 CC and stable integration occurs into the genome of this insect using the
 CC transposase enzyme. In particular, this gene transfer method uses the
 CC plasmid pigA3y3GFP which contains a Cyc1es GFP gene expressed under a
 CC silk worm actin promoter (A3 promoter) between a pair of inverted repeat
 CC sequences of the transposon piggyBac. This polypeptide sequence is the
 CC protein product from the pigA3y3GFP plasmid DNA that represents the
 CC silkworm actin promoter controlling expression of the Cyc1es GFP gene
 CC given in an exemplification of the invention. NOTE: This sequence is
 CC given as an embedded protein in the sequence listing and is not referred
 CC to further within the specification.
 XX
 SQ Sequence 310 AA;
 Query Match 100.0%; Score 82; DB 8; Length 310;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GRPRHQGVWVGWGQK 15
 DB 37 GRPRHQGVWVGWGQK 51
 RESULT 8
 ADM05323
 ID ADM05323 standard; protein; 342 AA.
 XX
 AC ADM05323;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 XX Human protein of the invention SEQ ID NO:4008.
 DE human; gene therapy; diagnostic marker; pharmaceutical.
 KW Homo sapiens.
 XX
 OS Homo sapiens.
 XX
 FN EP1347046-A1.
 XX
 PD 24-SEP-2003.
 XX
 PF 12-APR-2002; 2002EP-00008400.
 XX
 PR 22-MAR-2002; 2002JP-00137785.
 XX
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
 XX
 DR WPI; 2003-723558/69.
 DR N-PSDB; ADM02880.
 XX
 PT New polynucleotides and polypeptides are useful in gene therapy, for
 PT developing a diagnostic marker or medicines for regulating their
 PT expression and activity, or as a target of gene therapy.
 XX
 PS Claim 1; SEQ ID NO 4008; 305pp; English.
 XX
 CC The invention relates to a novel human polynucleotide and the encoded
 CC polypeptide. A polynucleotide of the invention may have a use in gene
 CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
 CC as a primer for synthesizing the polynucleotide or as a probe for

CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
 CC useful in gene therapy, for developing a diagnostic marker or medicines
 CC for regulating their expression and activity, or as a target of gene
 CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
 CC are useful as pharmaceutical agents. The present sequence represents a
 CC protein sequence of the invention.
 XX
 SQ Sequence 342 AA;
 Query Match 100.0%; Score 82; DB 7; Length 342;
 Best Local Similarity 100.0%; Pred. No. 1.7e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GRPRHQGVWVGWGQK 15
 DB 38 GRPRHQGVWVGWGQK 52
 RESULT 9
 AAB12985
 ID AAB12985 standard; protein; 374 AA.
 XX
 AC AAB12985;
 XX
 DT 29-NOV-2000 (first entry)
 XX
 XX Human beta-actin protein sequence.
 DE
 XX Beta actin; post translational modification; sickle cell anaemia;
 KW irreversibly sickled cell; ISC; treatment.
 XX
 OS Homo sapiens.
 XX
 FN US6087398-A.
 XX
 PD 11-JUL-2000.
 XX
 PF 01-MAR-1996; 96US-00609236.
 XX
 PR 14-AUG-1995; 95US-0002288P.
 XX
 PA (SALA-) SOUTH ALABAMA MEDICAL SCI FOUND.
 XX
 PI Goodman SR;
 XX
 DR WPI; 2000-498210/44.
 XX
 PT Treatment for sickle cell anemia comprises administering a reducing agent
 PT to inhibit and reverse sickled cell formation in blood.
 XX
 PS Example 17; Fig 5B; 53pp; English.
 XX
 CC This invention provides a treatment for sickle cell anaemia, which
 CC comprises administering a reducing agent. The treatment inhibits the
 CC formation of irreversible sickled cells (ISC) and reverses ISC formation
 CC in the blood. The present sequence represents the human beta-actin
 CC protein. The sequence is used in the invention to demonstrate that a
 CC disulphide bridge is formed between cysteines 284 and 373 in ISC beta-
 CC actin as a post-translational modification. The reducing agent used in
 CC the treatment acts to correct this post-translational modification
 XX
 SQ Sequence 374 AA;
 Query Match 100.0%; Score 82; DB 3; Length 374;
 Best Local Similarity 100.0%; Pred. No. 1.9e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GRPRHQGVWVGWGQK 15
 DB 35 GRPRHQGVWVGWGQK 49
 RESULT 10

CC analyses show that ACTC is linked to idiopathic dilated cardiomyopathy (IDC). The ACTC gene maps to chromosome 15q14. Six PCR primer pairs (AAA49020 to AAA49031) have been developed to allow analysis of the six exons of ACTC. Studies of two families with IDC showed the presence of two mutations, one in exon 5 and one in exon 6. The present sequence is a mutant of posttranslationally modified ACTC without the initial two residues. The mutation is a Glu to Gly mutation at position 361. The ACTC protein may be used in a variety of methods for drug screening and for rational drug design. The ACTC gene may be used to treat IDC by gene therapy. Analysis of the ACTC gene provides early identification of subjects likely to develop or who already have IDC. Note: The present sequence is not shown in the specification but is derived from the ACTC sequence described in AAY94569

XX SQ Sequence 375 AA;

Query Match 100.0%; Score 82; DB 3; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRPRHQGVVVGWGQK 15
|||||
Db 36 GRPRHQGVVVGWGQK 50

RESULT 13
AAY94569
ID AAY94569 standard; protein; 375 AA.
XX
AC AAY94569;
XX
DT 07-DEC-2000 (first entry)
XX Human cardiac actin protein after posttranslational modification.
DE
XX Cardiac actin; ACTC; human; gene therapy; IDC; 15q14;
KW idiopathic dilated cardiomyopathy.
XX
XX Homo sapiens.
XX US6063576-A.
XX 16-MAY-2000.
XX 29-JUN-1998; 98US-00106217.
XX 29-JUN-1998; 98US-00106217.
XX (UTAH) UNIV UTAH RES FOUND.
XX Olson TM, Keating MT;
XX WPI; 2000-375488/32.
XX N-PSDB; AAA49032.
XX New cardiac actin gene comprising histidine to arginine or glycine to glutamic acid substitution, useful in the diagnosis of diseases associated with the mutation, specifically idiopathic dilated cardiomyopathy.
XX Claim 3; Col 61-62; 36pp; English.
XX The present sequence is human cardiac actin (ACTC) protein, without the initial Met-Cys which is posttranslationally removed. Genotypic analyses show that ACTC is linked to idiopathic dilated cardiomyopathy (IDC). The ACTC gene maps to chromosome 15q14. Six PCR primer pairs (AAA49020 to AAA49031) have been developed to allow analysis of the six exons of ACTC. Studies of two families with IDC showed the presence of two mutations, one in exon 5 and one in exon 6. The mutations are G to A in codon 312 (Arg312His) and A to G in codon 361 (Glu361Gly). The ACTC protein may be used in a variety of methods for drug screening and for rational drug design. The ACTC gene may be used to treat IDC by gene therapy. Analysis of the ACTC gene provides early identification of subjects likely to

CC develop or who already have IDC
XX SQ Sequence 375 AA;

Query Match 100.0%; Score 82; DB 3; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRPRHQGVVVGWGQK 15
|||||
Db 36 GRPRHQGVVVGWGQK 50

RESULT 14
AAB15016
ID AAB15016 standard; protein; 375 AA.
XX
AC AAB15016;
XX
DT 07-DEC-2000 (first entry)
XX Posttranslationally modified human cardiac actin mutant R312H.
DE
XX Cardiac actin; ACTC; human; gene therapy; IDC; chromosome 15q14;
KW idiopathic dilated cardiomyopathy; mutant; mutein.
XX
XX Homo sapiens.
XX Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 312
FT /note= "Wild-type Arg substituted by His"
XX
XX US6063576-A.
XX 16-MAY-2000.
XX 29-JUN-1998; 98US-00106217.
XX 29-JUN-1998; 98US-00106217.
XX (UTAH) UNIV UTAH RES FOUND.
XX Olson TM, Keating MT;
XX WPI; 2000-375488/32.
XX N-PSDB; AAA73738.
XX New cardiac actin gene comprising histidine to arginine or glycine to glutamic acid substitution, useful in the diagnosis of diseases associated with the mutation, specifically idiopathic dilated cardiomyopathy.
XX Claim 3; Page; 36pp; English.
XX The present invention relates to human cardiac actin (ACTC). Genotypic analyses show that ACTC is linked to idiopathic dilated cardiomyopathy (IDC). The ACTC gene maps to chromosome 15q14. Six PCR primer pairs (AAA49020 to AAA49031) have been developed to allow analysis of the six exons of ACTC. Studies of two families with IDC showed the presence of two mutations, one in exon 5 and one in exon 6. The present sequence is a mutant of posttranslationally modified ACTC without the initial two residues. The mutation is a Arg to His mutation at position 312. The ACTC protein may be used in a variety of methods for drug screening and for rational drug design. The ACTC gene may be used to treat IDC by gene therapy. Analysis of the ACTC gene provides early identification of subjects likely to develop or who already have IDC. Note: The present sequence is not shown in the specification but is derived from the ACTC sequence described in AAY94569

XX SQ Sequence 375 AA;

Query Match 100.0%; Score 82; DB 3; Length 375;

Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRPRHQGVVGVGQK 15
Db 36 GRPRHQGVVGVGQK 50

RESULT 15

ABB77395
ID ABB77395 standard; protein; 375 AA.

XX AC ABB77395;

DT 11-JUL-2002 (first entry)

DE Human actin gamma 1.

XX Human; dermatological; skin stress; ageing; spondin 2; cathepsin L;
KW actin gamma 1; vimentin; fibroblast; skin; cosmetic; pharmaceutical.

XX OS Homo sapiens.

XX PN DE1050274-A1.

XX PD 18-APR-2002.

XX PF 09-OCT-2000; 2000DE-01050274.

XX PR 09-OCT-2000; 2000DE-01050274.

XX PA (HENK) HENKEL KGAA.

XX PI Petersohn D, Schmitt G, Foerster T;

XX DR WPI; 2002-373046/41.

XX PT In vitro assays for skin stress and skin ageing includes determination of
PT spondin 2, cathepsin L, actin gamma 1 and vimentin fragments secreted by
XX skin fibroblasts.

PS Claim 6; Page 12; 14pp; German.

XX The invention relates to in vitro methods for the detection of skin
CC stress and/or skin ageing in humans and animals based on the
CC determination of spondin 2, cathepsin L, actin gamma 1 or vimentin
CC fragments secreted by fibroblast from the skin under test. Use of the
CC methods in a test for potential cosmetics and pharmaceuticals with an
CC effect on these skin conditions and products containing vimentin
CC fragments are also included. Products containing vimentin fragments are
CC effective in the regulation, especially maintenance, of skin homeostasis

SQ Sequence 375 AA;

Query Match 100.0%; Score 82; DB 5; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRPRHQGVVGVGQK 15
Db 36 GRPRHQGVVGVGQK 50

Search completed: April 8, 2005, 10:50:42
Job time : 62.4 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:57 ; Search time 17.5333 Seconds
(without alignments)
63.863 Million cell updates/sec

Title: US-09-423-351C-3
Sequence: 82
1 GRPRHGVGMVGMGQK 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
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5: /cgn2_6/prodata/1/1aa/ECTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	100.0	20	US-08-505-250-17	Sequence 17, Appl
2	82	100.0	20	US-08-505-250-17	Sequence 17, Appl
3	82	100.0	374	US-08-609-236-6	Sequence 6, Appl
4	82	100.0	375	US-08-494-151-14	Sequence 14, Appl
5	82	100.0	375	US-09-106-217-16	Sequence 16, Appl
6	82	100.0	375	US-09-976-594-731	Sequence 731, Appl
7	82	100.0	376	US-08-588-113-2	Sequence 2, Appl
8	82	100.0	376	US-09-949-016-6100	Sequence 6100, Ap
9	82	100.0	377	US-09-106-217-2	Sequence 2, Appl
10	82	100.0	377	US-09-919-172-33	Sequence 33, Appl
11	82	100.0	377	US-09-917-254-53	Sequence 53, Appl
12	82	100.0	386	US-09-949-016-7721	Sequence 7721, Ap
13	82	100.0	399	US-09-949-016-9424	Sequence 9424, Ap
14	82	100.0	402	US-09-949-016-10757	Sequence 10757, A
15	82	100.0	404	US-09-949-016-11313	Sequence 11313, A
16	81	98.8	377	US-09-248-796A-14109	Sequence 14109, A
17	77	93.9	71	US-09-621-976-6521	Sequence 6521, Ap
18	76	92.7	374	US-09-306-446C-2	Sequence 2, Appl
19	75	91.5	375	US-09-171-337A-7	Sequence 7, Appl
20	75	91.5	375	US-09-171-337A-8	Sequence 8, Appl
21	75	91.5	375	US-09-631-022-7	Sequence 7, Appl
22	75	91.5	375	US-09-631-022-8	Sequence 8, Appl
23	47	57.3	397	US-09-902-540-9949	Sequence 9949, Ap
24	46	56.1	80	US-09-306-446C-4	Sequence 4, Appl
25	44	53.7	318	US-09-199-637A-23	Sequence 23, Appl
26	42	51.2	494	US-09-252-991A-32227	Sequence 32227, A
27	41.5	50.6	486	US-09-489-039A-10979	Sequence 10979, A

28	41	50.0	197	4	US-09-252-991A-32294	Sequence 32294, A
29	41	50.0	357	4	US-09-270-767-42609	Sequence 42609, A
30	41	50.0	376	4	US-09-538-092-1110	Sequence 1110, Ap
31	41	50.0	376	4	US-09-949-016-6656	Sequence 6656, Ap
32	41	50.0	376	4	US-09-949-016-8452	Sequence 8452, Ap
33	41	50.0	452	4	US-09-252-991A-23336	Sequence 23336, A
34	41	50.0	543	4	US-09-252-991A-18055	Sequence 18055, A
35	40	48.8	72	4	US-09-252-991A-28861	Sequence 28861, A
36	40	48.8	208	4	US-09-252-991A-19578	Sequence 19578, A
37	40	48.8	211	4	US-09-252-991A-18464	Sequence 18464, A
38	40	48.8	212	4	US-09-252-991A-29187	Sequence 29187, A
39	40	48.8	357	4	US-09-444-336-8	Sequence 8, Appl
40	40	48.8	357	4	US-09-444-336-9	Sequence 9, Appl
41	40	48.8	359	4	US-09-444-336-1	Sequence 1, Appl
42	40	48.8	362	4	US-09-444-336-2	Sequence 2, Appl
43	40	48.8	363	4	US-09-252-991A-27806	Sequence 27806, A
44	40	48.8	426	1	US-07-918-023-2	Sequence 2, Appl
45	40	48.8	599	4	US-09-949-016-8890	Sequence 8890, Ap

ALIGNMENTS

RESULT 1
US-08-505-250-17
; Sequence 17, Application US/08505250
; Patent No. 6183983
; GENERAL INFORMATION:
; APPLICANT: Sato, Haruya
; APPLICANT: Yamamoto, Keiji
; APPLICANT: Suzuki, Kokichi
; APPLICANT: Ikeda, Masahiro
; APPLICANT: Sakagami, Masahiro
; APPLICANT: Taniguchi, Makoto
; TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
; FILE REFERENCE: 110-511
; CURRENT APPLICATION NUMBER: US/08/505,250
; CURRENT FILING DATE: 1995-11-29
; EARLIER APPLICATION NUMBER: PCT/JP95/00298
; EARLIER FILING DATE: 1995-02-27
; EARLIER APPLICATION NUMBER: JP 198187/94
; EARLIER FILING DATE: 1994-08-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-08-505-250-17

Query Match 100.0%; Score 82; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRPRHGVGMVGMGQK 15
Db 5 GRPRHGVGMVGMGQK 19

RESULT 2
US-08-505-250-17
; Sequence 17, Application US/08505250
; Patent No. 6322996
; GENERAL INFORMATION:
; APPLICANT: Sato, Haruya
; APPLICANT: Yamamoto, Keiji
; APPLICANT: Suzuki, Kokichi
; APPLICANT: Ikeda, Masahiro
; APPLICANT: Sakagami, Masahiro
; APPLICANT: Taniguchi, Makoto

;; TITLE OF INVENTION: PROTEIN MODIFICATION METHOD

;; FILE REFERENCE: 110-511
 ;; CURRENT APPLICATION NUMBER: US/08/505,250
 ;; CURRENT FILING DATE: 1995-11-29
 ;; PRIOR APPLICATION NUMBER: PCT/JP95/00298
 ;; PRIOR FILING DATE: 1995-02-27
 ;; PRIOR APPLICATION NUMBER: JP 198187/94
 ;; PRIOR FILING DATE: 1994-08-23
 ;; NUMBER OF SEQ ID NOS: 53
 ;; SOFTWARE: PatentIn Ver. 2.0
 ;; SEQ ID NO 17
 ;; LENGTH: 20
 ;; TYPE: PRT
 ;; ORGANISM: Artificial Sequence
 ;; FEATURE:
 ;; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ;; OTHER INFORMATION: peptide
 US-08-505-250-17

Query Match 100.0%; Score 82; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRPRHQGVVMVGQK 15
 DB 5 GRPRHQGVVMVGQK 19

RESULT 3

US-08-609-236-6
 ; Sequence 6, Application US/08609236
 ; Patent No. 6087398

;; GENERAL INFORMATION:
 ;; APPLICANT: Steven R. Goodman
 ;; TITLE OF INVENTION: No. 6087398e1 Sickie Cell Anemia Treatment
 ;; NUMBER OF SEQUENCES: 6
 ;; CORRESPONDENCE ADDRESS:
 ;; ADDRESSEE: McGregor & Adler, LLP
 ;; STREET: 8011 Candle Lane
 ;; CITY: Houston
 ;; STATE: Texas
 ;; COUNTRY: USA
 ;; ZIP: 77071

;; COMPUTER READABLE FORM:
 ;; MEDIUM TYPE: Floppy disk
 ;; COMPUTER: Apple Macintosh
 ;; OPERATING SYSTEM: Macintosh
 ;; SOFTWARE: Microsoft Word for Macintosh
 ;; CURRENT APPLICATION DATA:
 ;; APPLICATION NUMBER: US/08/609,236
 ;; FILING DATE: March 1, 1996

;; CLASSIFICATION: 514
 ;; PRIOR APPLICATION DATA:
 ;; APPLICATION NUMBER: 60/002,288
 ;; FILING DATE: August 14, 1995
 ;; CLASSIFICATION: 514
 ;; ATTORNEY/AGENT INFORMATION:
 ;; NAME: Benjamin Aaron Adler, Ph.D.
 ;; REGISTRATION NUMBER: 35,423
 ;; REFERENCE/DOCKET NUMBER: D5807

;; TELECOMMUNICATION INFORMATION:
 ;; TELEPHONE: 713-777-2321
 ;; TELEFAX: 713-777-6908
 ;; INFORMATION FOR SEQ ID NO: 6:
 ;; SEQUENCE CHARACTERISTICS:
 ;; LENGTH: 374
 ;; TYPE: Amino acid
 ;; STRANDEDNESS:
 ;; TOPOLOGY: Linear
 ;; MOLECULE TYPE: Protein
 ;; DESCRIPTION: NO
 ;; HYPOTHETICAL: NO
 ;; ANTI-SENSE: NO

;; FRAGMENT TYPE:
 ;; ORIGINAL SOURCE:

;; STRAIN:
 ;; INDIVIDUAL ISOLATE:
 ;; DEVELOPMENTAL STAGE:
 ;; TISSUE TYPE:
 ;; CELL TYPE:
 ;; CELL LINE:
 US-08-609-236-6

Query Match 100.0%; Score 82; DB 3; Length 374;
 Best Local Similarity 100.0%; Pred. No. 4.8e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRPRHQGVVMVGQK 15
 DB 35 GRPRHQGVVMVGQK 49

RESULT 4

US-08-494-151-14
 ; Sequence 14, Application US/08494151
 ; Patent No. 5840528

;; GENERAL INFORMATION:
 ;; APPLICANT: Van Ooyen, Albert Johannes Joseph
 ;; TITLE OF INVENTION: Transformation of Phaffia rhodozyma
 ;; NUMBER OF SEQUENCES: 14
 ;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Morrison & Foerster
 ;; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
 ;; CITY: Washington, D.C.
 ;; COUNTRY: USA
 ;; ZIP: 20006-1812

;; COMPUTER READABLE FORM:
 ;; MEDIUM TYPE: Floppy disk
 ;; COMPUTER: IBM PC compatible
 ;; OPERATING SYSTEM: PC-DOS/MS-DOS
 ;; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ;; CURRENT APPLICATION DATA:
 ;; APPLICATION NUMBER: US/08/494,151
 ;; FILING DATE: 23-JUN-1995

;; CLASSIFICATION: 435
 ;; ATTORNEY/AGENT INFORMATION:
 ;; NAME: Murashige, Kate H.
 ;; REGISTRATION NUMBER: 29,959
 ;; REFERENCE/DOCKET NUMBER: 24615-20039.01
 ;; TELECOMMUNICATION INFORMATION:
 ;; TELEPHONE: (202) 887-1500
 ;; TELEFAX: (202) 887-0763
 ;; TELEX: 90-4030

;; INFORMATION FOR SEQ ID NO: 14:
 ;; SEQUENCE CHARACTERISTICS:
 ;; LENGTH: 375 amino acids
 ;; TYPE: amino acid
 ;; TOPOLOGY: linear
 ;; MOLECULE TYPE: protein
 US-08-494-151-14

Query Match 100.0%; Score 82; DB 2; Length 375;
 Best Local Similarity 100.0%; Pred. No. 4.8e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRPRHQGVVMVGQK 15
 DB 36 GRPRHQGVVMVGQK 50

RESULT 5

US-09-106-217-16
 ; Sequence 16, Application US/09106217
 ; Patent No. 6063576
 ;; GENERAL INFORMATION:
 ;; APPLICANT: Keating, Mark T.

APPLICANT: Olson, Timothy M.
TITLE OF INVENTION: Actin Mutations in Dilated
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
STREET: 555 Thirteenth Street, N.W., Suite 701 East
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,217
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 2323-125
TELEPHONE: 202-783-6040
TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-106-217-16

Query Match 100.0%; Score 82; DB 3; Length 375;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRPRHQGVVMGQK 15
Db 36 GRPRHQGVVMGQK 50

RESULT 6
US-09-976-594-731
Sequence 731, Application US/09976594
Patent No. 6673549
GENERAL INFORMATION:
APPLICANT: Furness, Michael
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
SEQ ID NO 731
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673549 1837317CD1
US-09-976-594-731

Query Match 100.0%; Score 82; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRPRHQGVVMGQK 15
Db 36 GRPRHQGVVMGQK 50

RESULT 7
US-08-588-113-2
Sequence 2, Application US/08588113
Patent No. 5710003
GENERAL INFORMATION:
APPLICANT: McHugh, Kirk M.
TITLE OF INVENTION: DIAGNOSTIC TEST FOR DETERMINING
MALIGNANCY OF SMOOTH MUSCLE TUMORS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 5710003ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: -US/08/588,113
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Ralph, Rebecca L.
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: T0U-1652
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-588-113-2

Query Match 100.0%; Score 82; DB 1; Length 376;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRPRHQGVVMGQK 15
Db 37 GRPRHQGVVMGQK 51

RESULT 8
US-09-949-016-6100
Sequence 6100, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6100
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6100

Query Match      100.0%; Score 82; DB 4; Length 376;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GRPRHQGVVMVGQK 15
Db      37 GRPRHQGVVMVGQK 51
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RESULT 9
US-09-106-217-2
; Sequence 2, Application US/09106217
; Patent No. 6063576
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Olson, Timothy M.
; TITLE OF INVENTION: Actin Mutations in Dilated
; TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,217
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 2323-125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-106-217-2

Query Match      100.0%; Score 82; DB 3; Length 377;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GRPRHQGVVMVGQK 15
Db      38 GRPRHQGVVMVGQK 52
|||||

RESULT 10
US-09-919-172-33
; Sequence 33, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Paris, Mary
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; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 33
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673545 1709118CD1
US-09-919-172-33

Query Match      100.0%; Score 82; DB 4; Length 377;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GRPRHQGVVMVGQK 15
Db      38 GRPRHQGVVMVGQK 52
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RESULT 11
US-09-917-254-53
; Sequence 53, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
; APPLICANT: Mutter, George
; APPLICANT: Baak, Jan
; TITLE OF INVENTION: Prognostic Classification of Breast Cancer
; FILE REFERENCE: B0801/7224(JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/222,093
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 53
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-917-254-53

Query Match      100.0%; Score 82; DB 4; Length 377;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GRPRHQGVVMVGQK 15
Db      38 GRPRHQGVVMVGQK 52
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RESULT 12
US-09-949-016-7721
; Sequence 7721, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7721
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7721

Query Match 100.0%; Score 82; DB 4; Length 386;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRPRHQGVVGMGQK 15
Db 47 GRPRHQGVVGMGQK 61

RESULT 13
US-09-949-016-9424
; Sequence 9424, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9424
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9424

Query Match 100.0%; Score 82; DB 4; Length 399;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRPRHQGVVGMGQK 15
Db 60 GRPRHQGVVGMGQK 74

RESULT 14
US-09-949-016-10757
; Sequence 10757, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10757
; LENGTH: 402

; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10757

Query Match 100.0%; Score 82; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRPRHQGVVGMGQK 15
Db 63 GRPRHQGVVGMGQK 77

RESULT 15
US-09-949-016-11313
; Sequence 11313, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11313
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11313

Query Match 100.0%; Score 82; DB 4; Length 404;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRPRHQGVVGMGQK 15
Db 65 GRPRHQGVVGMGQK 79

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OM protein - protein search, using sw model

Run on: April 8, 2005, 10:53:18 ; Search time 42.6667 Seconds
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Perfect score: 82
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Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA:*
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 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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 - 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
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 - 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
 - 17: /cgn2_6/ptodata/1/pubpaa/US10D_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
 - 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
 - 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	100.0	105	15	US-10-264-049-3601
2	82	100.0	142	15	US-10-424-599-184471
3	82	100.0	201	15	US-10-264-049-4308
4	82	100.0	204	15	US-10-264-049-4148
5	82	100.0	219	14	US-10-002-631C-56
6	82	100.0	342	15	US-10-108-260A-4008
7	82	100.0	371	16	US-10-322-281-68
8	82	100.0	375	14	US-10-205-194-93
9	82	100.0	375	14	US-10-316-253-88
10	82	100.0	375	15	US-10-369-493-5927
11	82	100.0	375	15	US-10-205-331-94
12	82	100.0	375	15	US-10-260-708-82
13	82	100.0	376	15	US-10-341-434-101
					Sequence 3601, Ap
					Sequence 184471, Ap
					Sequence 4308, Ap
					Sequence 4148, Ap
					Sequence 56, Appl
					Sequence 4008, Ap
					Sequence 68, Appl
					Sequence 93, Appl
					Sequence 86, Appl
					Sequence 5927, Ap
					Sequence 94, Appl
					Sequence 82, Appl
					Sequence 101, Appl

- Sequence 33, Appl
- Sequence 64, Appl
- Sequence 4, Appl
- Sequence 63, Appl
- Sequence 1436, Ap
- Sequence 1786, Ap
- Sequence 1, Appl
- Sequence 32056, A
- Sequence 310, App
- Sequence 161245, A
- Sequence 35226, A
- Sequence 47318, A
- Sequence 280811, A
- Sequence 280810, A
- Sequence 282905, A
- Sequence 42770, A
- Sequence 162684, A
- Sequence 28333, A
- Sequence 2436, Ap
- Sequence 179917, A
- Sequence 202420, A
- Sequence 45677, A
- Sequence 46090, A
- Sequence 52, Appl
- Sequence 162009, A
- Sequence 162685, A
- Sequence 162686, A
- Sequence 222816, A
- Sequence 223492, A
- Sequence 283336, A
- Sequence 66124, A
- Sequence 121952, A

ALIGNMENTS

RESULT 1
US-10-264-049-3601
; Sequence 3601, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA13321
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 3601
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (103)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-3601

Query Match 100.0%; Score 82; DB 15; Length 105;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRPRHQGVWVGWQK 15
Db 37 GRPRHQGVWVGWQK 51

RESULT 2

```

; LOCATION: (145)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (151)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (159)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (172)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (174)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (180)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
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US-10-264-049-4308

Query Match 100.0%; Score 82; DB 15; Length 201;
Best Local Similarity 100.0%; Pred. No. 9.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRPRHQGVVMVGQK 15
Db 53 GRPRHQGVVMVGQK 67
|||||
|||||

RESULT 4
US-10-264-049-4148
; Sequence 4148, Application US/10264049
; Publication No. US2004000579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4148
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-10-264-049-4148

Query Match 100.0%; Score 82; DB 15; Length 204;
Best Local Similarity 100.0%; Pred. No. 9.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRPRHQGVVMVGQK 15
Db 56 GRPRHQGVVMVGQK 70
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RESULT 5
US-10-002-631C-56
; Sequence 56, Application US/10002631C
; Publication No. US20030157486A1
; GENERAL INFORMATION:
; APPLICANT: Graff, Jonathon M.
; APPLICANT: Muenster, Matthew
; TITLE OF INVENTION: METHODS TO IDENTIFY SIGNAL SEQUENCES
; FILE REFERENCE: A34943 090495.0243

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; CURRENT APPLICATION NUMBER: US/10/002,631C
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/300,309
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-631C-56

Query Match      100.0%; Score 82; DB 14; Length 219;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GRPRHQGVVMVGQK 15
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Db      63 GRPRHQGVVMVGQK 77

RESULT 6
US-10-108-260A-4008
; Sequence 4008, Application US/10108260A
; Publication NO. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: HL-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4008
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-4008

Query Match      100.0%; Score 82; DB 15; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GRPRHQGVVMVGQK 15
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Db      38 GRPRHQGVVMVGQK 52

RESULT 7
US-10-322-281-68
; Sequence 68, Application US/10322281
; Publication NO. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-281-68

Query Match      100.0%; Score 82; DB 16; Length 371;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GRPRHQGVVMVGQK 15
       |||||

; CURRENT APPLICATION NUMBER: US/10/002,631C
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/300,309
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-631C-56

Query Match      100.0%; Score 82; DB 14; Length 219;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GRPRHQGVVMVGQK 15
       |||||
Db      63 GRPRHQGVVMVGQK 77

RESULT 8
US-10-205-194-93
; Sequence 93, Application US/10205194
; Publication NO. US20030134301A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Finnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018201
; CURRENT APPLICATION NUMBER: US/10/205,194
; CURRENT FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Rattus rattus
; OTHER INFORMATION: Cytoplasmic gamma isoform of actin
US-10-205-194-93

Query Match      100.0%; Score 82; DB 14; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GRPRHQGVVMVGQK 15
       |||||
Db      36 GRPRHQGVVMVGQK 50

RESULT 9
US-10-316-253-88
; Sequence 88, Application US/10316253
; Publication NO. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-88

Query Match      100.0%; Score 82; DB 14; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GRPRHQGVVMVGQK 15
       |||||
Db      36 GRPRHQGVVMVGQK 50

RESULT 10
US-10-369-493-5927
```

; Sequence 5927, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xiaofeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5927
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5927

Query Match 100.0%; Score 82; DB 15; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRPRHQGVWVGWQK 15
|||
Db 36 GRPRHQGVWVGWQK 50

RESULT 11
US-10-205-331-94
; Sequence 94, Application US/10205331
; Publication No. US20040058326A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pinnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018199
; CURRENT APPLICATION NUMBER: US/10/205,331
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 94
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Cytoplasmic beta-actin
US-10-205-331-94

Query Match 100.0%; Score 82; DB 15; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRPRHQGVWVGWQK 15
|||
Db 36 GRPRHQGVWVGWQK 50

RESULT 12
US-10-260-708-82
; Sequence 82, Application US/10260708
; Publication No. US20040063101A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Lee, Sang-Yull

; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: Human Sarcoma-Associated Antigens
; FILE REFERENCE: L00461/70138
; CURRENT APPLICATION NUMBER: US/10/260,708
; CURRENT FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 375
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-260-708-82

Query Match 100.0%; Score 82; DB 15; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRPRHQGVWVGWQK 15
|||
Db 36 GRPRHQGVWVGWQK 50

RESULT 13
US-10-341-434-101
; Sequence 101, Application US/10341434
; Publication No. US20030215835A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
; FILE REFERENCE: 9U 204 205 R1
; CURRENT APPLICATION NUMBER: US/10/341,434
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/348,164
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 60/348,119
; PRIOR FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-341-434-101

Query Match 100.0%; Score 82; DB 15; Length 376;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRPRHQGVWVGWQK 15
|||
Db 37 GRPRHQGVWVGWQK 51

RESULT 14
US-09-919-172-33
; Sequence 33, Application US/09919172
; Patent No. US20020119463A1
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 33
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20020119463A1 1709118CD1
US-09-919-172-33

Query Match 100.0%; Score 82; DB 9; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRPRHQGVVGMGQK 15
Db 38 GRPRHQGVVGMGQK 52

RESULT 15
US-10-236-031B-64
; Sequence 64, Application US/10236031B
; Publication No. US20030219760A1
; GENERAL INFORMATION:
; APPLICANT: Gordon, Gavin J.
; APPLICANT: Jensen, Roderick V.
; APPLICANT: Gullans, Steven R.
; APPLICANT: Bueno, Raphael
; TITLE OF INVENTION: Diagnostic and Prognostic Tests
; FILE REFERENCE: B00801/70265 (JRV/JAV)
; CURRENT APPLICATION NUMBER: US/10/236,031B
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/317,389
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/407,431
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-031B-64

Query Match 100.0%; Score 82; DB 15; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRPRHQGVVGMGQK 15
Db 38 GRPRHQGVVGMGQK 52

Search completed: April 8, 2005, 12:50:57
Job time : 42.6667 secs

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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 9.33333 Seconds
(without alignments)
154.634 Million cell updates/sec

Title: US-09-423-351C-3
Perfect score: 82
Sequence: 1 GRPRHQGVWVGWGQK 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	100.0	86	C43616	actin beta, cytosol
2	82	100.0	137	A28258	actin 5C - fruit f
3	82	100.0	158	I49465	alpha-cardiac acti
4	82	100.0	213	A61043	actin CAL5 - sea s
5	82	100.0	308	A03000	actin 3 - fruit fl
6	82	100.0	328	S05430	actin beta - grass
7	82	100.0	349	B25819	actin, fetal skele
8	82	100.0	362	A26559	actin type 5, cyto
9	82	100.0	374	ATBOB	actin beta - bovin
10	82	100.0	374	ATBOG	actin gamma - bovi
11	82	100.0	374	JCS818	gamma-actin - huma
12	82	100.0	375	ATBOSM	actin, aortic smoo
13	82	100.0	375	ATRB	actin, skeletal mu
14	82	100.0	375	ATRTC	actin beta - rat
15	82	100.0	375	A48324	actin beta, cytosol
16	82	100.0	375	ATCHB	actin beta - chick
17	82	100.0	375	ATHUB	actin beta - human
18	82	100.0	375	ATHUG	actin gamma 1 - hu
19	82	100.0	375	ATMSB	actin beta - mouse
20	82	100.0	375	ATMSG	actin gamma - mous
21	82	100.0	375	ATRB	actin beta, non-mu
22	82	100.0	375	S11222	actin gamma, cytos
23	82	100.0	375	T25272	hypothetical prote
24	82	100.0	375	S71125	actin beta-2, cyto
25	82	100.0	375	S71124	actin beta-1, cyto
26	82	100.0	375	S71126	actin beta, cytosol
27	82	100.0	375	A55001	actin beta - goose
28	82	100.0	375	A54728	actin alpha, cardi
29	82	100.0	375	S70377	actin - Phaffia rh

30	82	100.0	376	1	ATFF7	actin 7 - fruit fl
31	82	100.0	376	1	A43552	actin gamma, cytos
32	82	100.0	376	1	ATCHSM	actin gamma, smoot
33	82	100.0	376	1	ATFF8	actin 8 - fruit fl
34	82	100.0	376	1	ATURS	actin Cy1 - sea ur
35	82	100.0	376	2	A48449	Actin-1A - nematoe
36	82	100.0	376	2	S04538	actin 87E - fruit
37	82	100.0	376	2	JC1246	actin - fruit fly
38	82	100.0	376	2	JS0189	actin, cytosolic -
39	82	100.0	376	2	JS0190	actin, muscle - st
40	82	100.0	376	2	S07288	actin 15A - sea ur
41	82	100.0	376	2	S09578	actin - sea urchin
42	82	100.0	376	2	A40261	actin gamma, enter
43	82	100.0	376	2	JQ0154	actin - Hydra atte
44	82	100.0	376	2	JN0832	actin (clone gen3)
45	82	100.0	376	2	JN0833	actin (clones Ia a

ALIGNMENTS

RESULT 1

C43616
actin beta, cytosolic - chicken (fragment)
C/Species: Gallus gallus (Chicken)
C/Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
C/Accession: C43616
R/Paterson, B.M.; Eldridge, J.D.
Science 224, 1436-1438, 1984
A/Title: Alpha-Cardiac actin is the major sarcomeric isoform expressed in embryonic avia
A/Reference number: A43616; MUID:84223949; PMID:6729461
A/Accession: C43616
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-86 <PAR>
A/Cross-references: UNIPROT:Q90736; GB:K02173; NID:g211054; PIDN:AAA98513.1; PID:g211055
C/Superfamily: actin
C/Keywords: cytosol; methylated amino acid
F,7/3/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 82; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRPRHQGVWVGWGQK 15
Db 36 GRPRHQGVWVGWGQK 50

RESULT 2

A28258
actin 5C - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C/Accession: A28258
R/Vigoreaux, J.O.; Tobin, S.L.
Genes Dev. 1, 1161-1171, 1987
A/Title: Stage-specific selection of alternative transcriptional initiation sites from
A/Reference number: A28258; MUID:88112795; PMID:3123314
A/Accession: A28258
A/Molecule type: mRNA
A/Residues: 1-137 <VIG>
A/Cross-references: UNIPROT:P10987
A/Note: the authors translated the codon GAG for residue 96 as Gly
C/Genetics:
A/Gene: FlyBase:Act5C
A/Cross-references: FlyBase:FBgn0000042
C/Superfamily: actin
C/Keywords: methylated amino acid
F,7/4/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 82; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRPRHQGVWVGQK 15
 |||||
 Db 37 GRPRHQGVWVGQK 51

RESULT 3
 I49465
 alpha-cardiac actin - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C:Accession: I49465; I49466
 R:Garner, I.; Minty, A.J.; Alonso, S.; Barton, P.J.R.; Buckingham, M.E.
 EMBL J. 5, 2559-2567, 1986
 A>Title: A 5' duplication of the alpha-cardiac actin gene in BALB/c mice is associated w
 A:Reference number: I49465; MUID:87053822; PMID:3023046
 A:Accession: I49465
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-158 <RES>
 A:CROSS-references: UNIPROT:Q61273; GB:M26775; NID:gl91646; PIDN:AAA37165.1; PID:g553858
 A:Accession: I49466
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 8-158 <RE2>
 A:CROSS-references: GB:M26776; NID:gl91649; PIDN:AAA37166.1; PID:g553859
 A:Experimental source: adult cardiac muscle, BALB/c mice
 C:Genetics:
 A:Introns: 50/3
 C:Superfamily: actin
 C:Keywords: cardiac muscle; heart

Query Match 100.0%; Score 82; DB 2; Length 158;
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRPRHQGVWVGQK 15
 |||||
 Db 45 GRPRHQGVWVGQK 59

RESULT 4
 A61043
 actin CA15 - sea squirt (Styela clava) (fragments)
 C:Species: Styela clava
 C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C:Accession: A61043
 R:Beach, R.L.; Jeffery, W.R.
 Dev. Genet. 11, 2-14, 1990
 A>Title: Temporal and spatial expression of a cytoskeletal actin gene in the ascidian St
 A:Reference number: A61043; MUID:90298580; PMID:2361333
 A:Accession: A61043
 A>Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-213 <BEA>
 A:CROSS-references: UNIPROT:Q7M3Y7
 C:Comment: This sequence is expressed in cells undergoing rapid cell division.
 C:Superfamily: actin
 C:Keywords: cytoskeleton; methylated amino acid; mitosis; structural protein
 F:73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 82; DB 2; Length 213;
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRPRHQGVWVGQK 15
 |||||
 Db 36 GRPRHQGVWVGQK 50

RESULT 5
 A03000

actin 3 - fruit fly (Drosophila melanogaster) (fragments)
 C:Species: Drosophila melanogaster
 C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
 C:Accession: A03000
 R:Fyrberg, E.A.; Bond, B.J.; Hershey, N.D.; Mixter, K.S.; Davidson, N.
 Cell 24, 107-116, 1981
 A>Title: The actin genes of Drosophila: protein coding regions are highly conserved but
 A:Reference number: A03000; MUID:81210174; PMID:6263481
 A:Accession: A03000
 A:Molecule type: DNA
 A:Residues: 1-308 <FYR>
 A:CROSS-references: UNIPROT:P02572
 A>Note: there are 68 unsequenced residues between positions 160 and 161. Partial sequenc
 A>Note: the authors translated the codon GTT for residue 263 as Ile
 C:Genetics:
 A:Gene: FlyBase:Act42A
 A:CROSS-references: FlyBase:FBgn0000043
 A:Map position: 42A
 C:Superfamily: actin
 C:Keywords: methylated amino acid
 F:74/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 82; DB 2; Length 308;
 Best Local Similarity 100.0%; Pred. No. 2.5e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRPRHQGVWVGQK 15
 |||||
 Db 37 GRPRHQGVWVGQK 51

RESULT 6
 S05430
 actin beta - grass carp
 C:Species: Ctenopharyngodon idella (grass carp)
 C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
 C:Accession: S05430
 R:Liu, Z.; Zhu, Z.; Roberg, K.; Faras, A.J.; Guise, K.S.; Kapuscinski, A.R.; Hackett, P.
 Nucleic Acids Res. 17, 5950, 1989
 A>Title: The beta-actin gene of carp (Ctenopharyngodon idella).
 A:Reference number: S05430; MUID:89345185; PMID:2762162
 A:Accession: S05430
 A>Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-328 <LIU>
 A:CROSS-references: UNIPROT:P83751; EMBL:M25013
 C:Genetics:
 A:Introns: 41/3; 121/3; 268/1
 C:Superfamily: actin
 C:Keywords: cytoskeleton; methylated amino acid
 F:73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 82; DB 2; Length 328;
 Best Local Similarity 100.0%; Pred. No. 2.7e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRPRHQGVWVGQK 15
 |||||
 Db 36 GRPRHQGVWVGQK 50

RESULT 7
 B25819
 actin, fetal skeletal/adult cardiac muscle - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 09-Jul-2004
 C:Accession: B25819
 R:Alonso, S.; Minty, A.; Bourlet, Y.; Buckingham, M.
 J. Mol. Evol. 23, 11-22, 1986
 A>Title: Comparison of three actin-coding sequences in the mouse; evolutionary relations
 A:Reference number: B25819; MUID:86200234; PMID:3084797
 A:Accession: B25819
 A:Molecule type: mRNA

A:Residues: 1-349 <ALO>
 A:Cross-references: UNIPROT:061275; GB:X03767; GB:J00381; GB:M10652; NID:G49869; PIDN:CA
 C:Superfamily: actin
 C:Keywords: cardiac muscle; heart; methylated amino acid; muscle; skeletal muscle
 F:47/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 82; DB 2; Length 349;
 Best Local Similarity 100.0%; Pred. No. 2.8e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRPRHQGVWVGQK 15
 |||||
 DB 10 GRPRHQGVWVGQK 24
 |||||

RESULT 8

A26559
 actin type 5, cytosolic - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 09-Sep-1987 #sequence_revision 09-Sep-1987 #text_change 05-Dec-1997
 A:Accession: A26559

R:Berghsma, D.J.; Chang, K.S.; Schwartz, R.J.
 Mol. Cell. Biol. 5, 1151-1162, 1985

A:Reference number: A26559; MUID:85213487; PMID:4000121

A:Accession: A26559

A:Molecule type: DNA

A:Residues: 1-362 <BER>

C:Superfamily: actin

C:Keywords: cytosol; methylated amino acid

F:74/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 82; DB 2; Length 362;
 Best Local Similarity 100.0%; Pred. No. 3e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRPRHQGVWVGQK 15
 |||||
 DB 37 GRPRHQGVWVGQK 51
 |||||

RESULT 9

ATBOG
 actin beta - bovine (tentative sequence)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004

C:Accession: E14185; A39105; A02999; A14185

R:Vandekerckhove, J.; Weber, K.

Eur. J. Biochem. 90, 451-462, 1978

A:Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain

A:Reference number: A14185; MUID:79045349; PMID:213279

A:Accession: E14185

A:Molecule type: protein

A:Residues: 1-374 <VAN>

A:Cross-references: UNIPROT:P60712

A:Note: Only peptides that differed in composition from the corresponding peptides of ra

R:Degen, J.L.; Neubauer, M.G.; Degen, S.J.F.; Seyfried, C.E.; Morris, D.R.

J. Biol. Chem. 258, 12153-12162, 1983

A:Title: Regulation of protein synthesis in mitogen-activated bovine lymphocytes. Analysis

A:Reference number: A39105; MUID:84032385; PMID:6195151

A:Accession: A39105

A:Molecule type: mRNA

A:Residues: 76-227;344-374 <DEG>

A:Cross-references: GB:K00622; GB:K00623

A:Note: actins beta and gamma were not distinguished in this study

C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,

C:Superfamily: actin

F:1/Modified site: blocked amino end (Asp) (probably acetylated) #status experimental

F:72/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 82; DB 1; Length 374;
 Best Local Similarity 100.0%; Pred. No. 3.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRPRHQGVWVGQK 15
 |||||
 DB 35 GRPRHQGVWVGQK 49
 |||||

RESULT 10

ATBOG
 actin gamma - bovine (tentative sequence)

C:Species: Bos primigenius taurus (cattle)

C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004

C:Accession: E14185; A02999

R:Vandekerckhove, J.; Weber, K.

Eur. J. Biochem. 90, 451-462, 1978

A:Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain

A:Reference number: A14185; MUID:79045349; PMID:213279

A:Accession: E14185

A:Molecule type: protein

A:Residues: 1-374 <VAN>

A:Cross-references: UNIPROT:P02571

A:Note: Only peptides that differed in composition from the corresponding peptides of ra

C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,

C:Superfamily: actin

C:Keywords: blocked amino end; cell motility; cytoskeleton; methylated amino acid; micro

F:1/Modified site: blocked amino end (Glu) (probably acetylated) #status experimental

F:72/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 82; DB 1; Length 374;
 Best Local Similarity 100.0%; Pred. No. 3.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRPRHQGVWVGQK 15
 |||||
 DB 35 GRPRHQGVWVGQK 49
 |||||

RESULT 11

JC5818
 gamma-actin - human

C:Species: Homo sapiens (man)

C:Date: 20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004

C:Accession: JC5818; PC4501

R:Haenschildt, S.; Schwarz, C.; Heine, H.; Ulmer, A.J.; Flad, H.D.; Rietschel, E.T.; Jens

Biochem. Biophys. Res. Commun. 241, 670-674, 1997

A:Title: Actin: A target of lipopolysaccharide-induced phosphorylation in human monocytes

A:Reference number: JC5818; MUID:98096379; PMID:9434766

A:Accession: JC5818

A:Molecule type: protein

A:Residues: 1-374 <HAU>

A:Experimental source: monocyte

A:Accession: PC4501

A:Molecule type: protein

A:Residues: 1-61;84-112;147-190;196-209;215-253;335-358 <HA2>

A:Experimental source: monocyte

C:Comment: This protein is involved in a signal transduction that eventually leads to mo

C:Superfamily: actin

Query Match 100.0%; Score 82; DB 2; Length 374;
 Best Local Similarity 100.0%; Pred. No. 3.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRPRHQGVWVGQK 15
 |||||
 DB 35 GRPRHQGVWVGQK 49
 |||||

RESULT 12

ATBOG

actin, aortic smooth muscle - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 06-Sep-1996

C:Accession: A02997; S13480

A/NOTE: THE SUBJECTS RATED TO TRANSLATED THE LOGON FOR 100% TO 100% AS 100%

C;Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
C;Genetics:
A;Introns: 41/3; 121/3; 268/3; 328/3
C;Superfamily: actin
C;Keywords: acetylated amino end; cell motility; cytoskeleton; methylated amino acid; mi
F;2-375/Product: actin beta, cytoskeletal #status predicted <MAT>
F;2/Modified site: acetylated amino end (Asp) (in mature form) #status predicted
F;73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 82; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRPRHQGVVGVGQK 15
| | | | | | | | | | | | | | | |
Db 36 GRPRHQGVVGVGQK 50

Search completed: April 8, 2005, 10:53:05
Job time : 10.3333 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 57.8667 Seconds
(without alignments)
132.739 Million cell updates/sec

Title: US-09-423-351C-3

Perfect score: 82
Sequence: 1 GRPRHQGVWVGWQK 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	82	100.0	26	2 Q6Q298	Q6Q298 ovis aries
2	82	100.0	53	2 Q6AW41	Q6AW41 bombyx mori
3	82	100.0	78	2 Q61375	Q61375 schmidtea p
4	82	100.0	78	2 Q61376	Q61376 schmidtea p
5	82	100.0	78	2 Q61377	Q61377 schmidtea p
6	82	100.0	79	2 Q95L83	Q95L83 oryctolagus
7	82	100.0	80	2 Q9TTW4	Q9TTW4 bos taurus
8	82	100.0	86	2 Q90736	Q90736 gallus gall
9	82	100.0	91	2 Q7Z211	Q7Z211 salvelinus
10	82	100.0	96	2 Q86CV4	Q86CV4 drosophila
11	82	100.0	96	2 Q86FV7	Q86FV7 drosophila
12	82	100.0	99	2 Q9QZB4	Q9QZB4 cavia porce
13	82	100.0	104	2 Q86SB7	Q86SB7 gryllus bim
14	82	100.0	108	2 Q18548	Q18548 lytechinus
15	82	100.0	108	2 Q18550	Q18550 lytechinus
16	82	100.0	117	2 Q8T6P7	Q8T6P7 elysia chlo
17	82	100.0	121	2 Q8JG71	Q8JG71 oreochromis
18	82	100.0	121	2 Q78CQ1	Q78CQ1 pseudopleur
19	82	100.0	129	2 Q6VBE4	Q6VBE4 locusta mig
20	82	100.0	130	2 Q93298	Q93298 pseudopleur
21	82	100.0	139	2 Q9DFK2	Q9DFK2 gillichthys
22	82	100.0	144	2 Q90YX9	Q90YX9 fundulus he
23	82	100.0	150	2 Q804Y9	Q804Y9 ictalurus p
24	82	100.0	151	2 Q61274	Q61274 mus musculu
25	82	100.0	151	2 Q9PSV5	Q9PSV5 oryzias lat
26	82	100.0	158	2 Q61273	Q61273 mus musculu
27	82	100.0	164	1 ACT SPOLI	Q11212 spodoptera
28	82	100.0	165	2 Q17477	Q17477 halictis ru
29	82	100.0	181	2 Q8JG41	Q8JG41 dicentrarch
30	82	100.0	181	2 Q8AWC8	Q8AWC8 chionodraco
31	82	100.0	181	2 Q8AWZ3	Q8AWZ3 argyropelec

32	82	100.0	181	2 Q9DEU3	Q9DEU3 scophthalmu
33	82	100.0	184	2 Q11209	Q11209 canis famil
34	82	100.0	186	2 Q8X190	Q8X190 paxillus in
35	82	100.0	189	2 Q8SPX4	Q8SPX4 canis famil
36	82	100.0	191	2 Q84G12	Q84G12 oxyuranus s
37	82	100.0	198	2 Q8Y250	Q8Y250 pagrus majo
38	82	100.0	202	2 Q810R5	Q810R5 mus musculu
39	82	100.0	212	2 Q6ZYL2	Q6ZYL2 arion lusit
40	82	100.0	213	2 Q7M3Y7	Q7M3Y7 styela clav
41	82	100.0	225	2 Q84G13	Q84G13 oxyuranus s
42	82	100.0	235	2 Q7XB23	Q7XB23 lotharella
43	82	100.0	235	2 Q7XB24	Q7XB24 lotharella
44	82	100.0	235	2 Q7XB25	Q7XB25 lotharella
45	82	100.0	236	2 Q6RXK3	Q6RXK3 penaeus van

ALIGNMENTS

RESULT 1

Q6Q298 PRELIMINARY; PRT; 26 AA.
AC Q6Q298;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DE Beta actin (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Abomasum;
RA Shanmuganathan T., Hickford J.G.H., Savill M., Sykes A.R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY566300; AAS68014.1; -.
FT NON_TER 1
FT NON_TER 26
SQ SEQUENCE 26 AA; 2802 MW; C75DA20C92E36C4B CRC64;

Query Match 100.0%; Score 82; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRPRHQGVWVGWQK 15
Db 7 GRPRHQGVWVGWQK 21

RESULT 2

Q6AW41 PRELIMINARY; PRT; 53 AA.
ID Q6AW41;
AC Q6AW41;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Cytoplasmic actin (Fragment).
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Daizo; TISSUE=Silk gland;
RA Shiomi K., Kajiuira Z., Nakagaki M., Yamashita O.;
RT "Baculovirus-mediated efficient gene transfer into the central nervous system of the silkworm, Bombyx mori.";
RL Nihon Sankigaku Zasshi 72:149-155(2003).
RN [2]
RP SEQUENCE FROM N.A.

```

RC STRAIN=Daizo; TISSUE=Silk gland;
RA Shiomi K.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB186491; BAD35130.1; -.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 53
SQ SEQUENCE 53 AA; 5465 MW; 227AA8B4872EBA86 CRC64;

Query Match 100.0%; Score 82; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRPRHQGVWVGQK 15
Db 37 GRPRHQGVWVGQK 51

RESULT 3
O61375 PRELIMINARY; PRT; 78 AA.
AC O61375;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Actin 1 (Fragment).
GN Name=DpAct1;
OS Schmidtea polychroa.
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC Paludicola; Dugesidae; Schmidtea.
OX NCBI_TaxID=50054;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98186847; PubMed=9518500; DOI=10.1093/nar/26.8.2031;
RA Fagotti A., Gabbiani G., Pascolini R., Neuville P.;
RT "Multiple isoform recovery (MIR)-PCR: a simple method for the
isolation of related mRNA isoforms.";
RL Nucleic Acids Res. 26:2031-2033(1998).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
in various types of cell motility and are ubiquitously expressed
in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AF027162; AAC38982.1; -.
DR HSSP; P02577; INMI.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
KW Structural protein.
FT NON_TER 78
SQ SEQUENCE 78 AA; 8265 MW; B9DF9B28E54ADB0E CRC64;

Query Match 100.0%; Score 82; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 4.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRPRHQGVWVGQK 15
Db 37 GRPRHQGVWVGQK 51

RESULT 5
O61377 PRELIMINARY; PRT; 78 AA.
AC O61377;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Actin 3 (Fragment).
GN Name=DpAct3;
OS Schmidtea polychroa.
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC Paludicola; Dugesidae; Schmidtea.
OX NCBI_TaxID=50054;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98186847; PubMed=9518500; DOI=10.1093/nar/26.8.2031;
RA Fagotti A., Gabbiani G., Pascolini R., Neuville P.;
RT "Multiple isoform recovery (MIR)-PCR: a simple method for the
isolation of related mRNA isoforms.";
RL Nucleic Acids Res. 26:2031-2033(1998).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
in various types of cell motility and are ubiquitously expressed
in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AF027161; AAC38981.1; -.
DR HSSP; P02577; INMI.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
KW Structural protein.
FT NON_TER 78
SQ SEQUENCE 78 AA; 8205 MW; 572BAB2698C24404 CRC64;

Query Match 100.0%; Score 82; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 4.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRPRHQGVWVGQK 15
Db 37 GRPRHQGVWVGQK 51

RESULT 4
O61376 PRELIMINARY; PRT; 78 AA.
AC O61376;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Actin 2 (Fragment).

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```

GN Name=DpAct2;
OS Schmidtea polychroa.
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC Paludicola; Dugesidae; Schmidtea.
OX NCBI_TaxID=50054;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98186847; PubMed=9518500; DOI=10.1093/nar/26.8.2031;
RA Fagotti A., Gabbiani G., Pascolini R., Neuville P.;
RT "Multiple isoform recovery (MIR)-PCR: a simple method for the
isolation of related mRNA isoforms.";
RL Nucleic Acids Res. 26:2031-2033(1998).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
in various types of cell motility and are ubiquitously expressed
in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AF027162; AAC38982.1; -.
DR HSSP; P02577; INMI.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
KW Structural protein.
FT NON_TER 78
SQ SEQUENCE 78 AA; 8265 MW; B9DF9B28E54ADB0E CRC64;

Query Match 100.0%; Score 82; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 4.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRPRHQGVWVGQK 15
Db 37 GRPRHQGVWVGQK 51

RESULT 5
O61377 PRELIMINARY; PRT; 78 AA.
AC O61377;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Actin 3 (Fragment).
GN Name=DpAct3;
OS Schmidtea polychroa.
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC Paludicola; Dugesidae; Schmidtea.
OX NCBI_TaxID=50054;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98186847; PubMed=9518500; DOI=10.1093/nar/26.8.2031;
RA Fagotti A., Gabbiani G., Pascolini R., Neuville P.;
RT "Multiple isoform recovery (MIR)-PCR: a simple method for the
isolation of related mRNA isoforms.";
RL Nucleic Acids Res. 26:2031-2033(1998).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
in various types of cell motility and are ubiquitously expressed
in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AF027163; AAC38983.1; -.
DR HSSP; P02577; INMI.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.

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KW Structural protein.
FT NON TER 78
SQ SEQUENCE 78 AA; 8299 MW; B9DFE1108E4ADBOE CRC64;

Query Match 100.0%; Score 82; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 4.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRPRHQGVVGMGQK 15
    |||||
Db 37 GRPRHQGVVGMGQK 51

RESULT 6
Q95L83 ID Q95L83 PRELIMINARY; PRT; 79 AA.
AC Q95L83;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Beta-actin (Fragment)
OS Oryctolagus cuniculus (Rabbit)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A. PubMed=12380804;
RX MEDLINE=22306422;
RA Wang D.-A., Du H., Jaggar J.H., Brindley D.N., Tigyi G.J.,
RA Watsky M.A.;
RT "Injury-elicited differential transcriptional regulation of
RT phospholipid growth factor receptors in the cornea.";
RL Am. J. Physiol. Cell Physiol. 283:C1646-C1654(2002).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AF404278; AAL01885.1; -
DR HSSP; P02577; INMI.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PRO0190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
KW Structural protein.
FT NON TER 79
SQ SEQUENCE 79 AA; 8420 MW; 05056E4E2AC092F8 CRC64;

Query Match 100.0%; Score 82; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 4.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRPRHQGVVGMGQK 15
    |||||
Db 38 GRPRHQGVVGMGQK 52

RESULT 7
Q9TTW4 ID Q9TTW4 PRELIMINARY; PRT; 80 AA.
AC Q9TTW4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Beta actin (Fragment)
OS Bos taurus (Bovine)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
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OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA John S.J., Bilocheau-Goesels S.;
RL submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AF191490; AAF05984.1; -
DR HSSP; P02577; INMI.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PRO0190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
KW Structural protein.
FT NON TER 80
SQ SEQUENCE 80 AA; 9133 MW; 47354ABB7010668D CRC64;

Query Match 100.0%; Score 82; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 4.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRPRHQGVVGMGQK 15
    |||||
Db 2 GRPRHQGVVGMGQK 16

RESULT 8
Q90736 ID Q90736 PRELIMINARY; PRT; 86 AA.
AC Q90736;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Beta-actin (Fragment)
OS Gallus gallus (Chicken)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84223949; PubMed=6729461;
RA Paterson B.M., Eldridge J.D.;
RT "alpha-Cardiac actin is the major sarcomeric isoform expressed in
RT embryonic avian skeletal muscle.";
RL Science 254:1436-1438(1984).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; K02173; AAA98513.1; -
DR FIR; C43616; C43616.
DR HSSP; P02577; INMI.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PRO0190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
KW Structural protein.
FT NON TER 86
SQ SEQUENCE 86 AA; 9351 MW; A55285196A328E6E CRC64;

Query Match 100.0%; Score 82; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 4.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



```

QY 1 GRPRHQGVWVGWGQK 15
DB 37 GRPRHQGVWVGWGQK 51

RESULT 12
Q90ZB4 PRELIMINARY; PRT; 99 AA.
AC Q90ZB4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE Cytoplasmic actin (Fragment).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal gland;
RA Buelow H.E., Bernhardt R.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AF191277; AAF13923.1; -.
DR HSP; P02577; INM1.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
DR Structural protein.
KW NON_TER 99
SQ SEQUENCE 99 AA; 10973 MW; 0562B645E8DAF17B CRC64;

Query Match 100.0%; Score 82; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRPRHQGVWVGWGQK 15
DB 36 GRPRHQGVWVGWGQK 50

RESULT 13
Q86SB7 PRELIMINARY; PRT; 104 AA.
AC Q86SB7;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE Actin (Fragment).
GN Name=ACT;
OS Gryllus bimaculatus (Two-spotted cricket).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC Gryllus.
OX NCBI_TaxID=6999;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang H., Shimmyo Y., Hirose A., Mito T., Inoue Y., Ohuchi H.,
RA Loukeris T.G., Naji S.;
RT "Extrachromosomal transposition of the transposable element Minos
RT occurs in embryos of the cricket Gryllus bimaculatus.";
RL Dev. Growth Differ. 0:0-0(2002).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).

-!- SIMILARITY: Belongs to the actin family.
EMBL; AB087882; BAC55093.1; -.
HSP; P02577; INM1.
GO; GO:0005884; C:actin filament; IEA.
GO; GO:0003774; F:motor activity; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004001; Actin.
Pfam; PF00022; Actin; 1.
PRINTS; PR00190; ACTIN.
PROSITE; PS00406; ACTINS_1; 1.
Structural protein.
NON_TER 104
SEQUENCE 104 AA; 11511 MW; 332777A2B08669B0 CRC64;

Query Match 100.0%; Score 82; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 5.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRPRHQGVWVGWGQK 15
DB 37 GRPRHQGVWVGWGQK 51

RESULT 14
O18548 PRELIMINARY; PRT; 108 AA.
AC O18548;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DE Cytoplasmic actin LvC4 (Fragment).
GN Name=LvC4;
OS Lytechinus variegatus (Sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Temnopleuroidea; Toxopneustidae;
OC Lytechinus.
OX NCBI_TaxID=7654;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97333945; PubMed=9190067;
RA Kissinger J.C., Hahn J.H., Raff R.A.;
RT "Rapid evolution in a conserved gene family. Evolution of the actin
RT gene family in the sea urchin genus Helicidaris and related genera.";
RL Mol. Biol. Evol. 14:654-665(1997).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
-!- SIMILARITY: Belongs to the actin family.
EMBL; U82542; AAB66299.1; -.
HSP; P10983; LD4X.
GO; GO:0005884; C:actin filament; IEA.
GO; GO:0003774; F:motor activity; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004001; Actin.
Pfam; PF00022; Actin; 1.
PRINTS; PR00190; ACTIN.
PROSITE; PS00406; ACTINS_1; 1.
PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
Structural protein.
NON_TER 108
SEQUENCE 108 AA; 12094 MW; F670CB8A6CB3DAE CRC64;

Query Match 100.0%; Score 82; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRPRHQGVWVGWGQK 15
DB 23 GRPRHQGVWVGWGQK 37

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RESULT 15
ID O18550 PRELIMINARY; PRT; 108 AA.
AC O18550;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytoplasmic actin LVC2 (fragment).
GN Name=Lvc2;
OS Lytechinus variegatus (Sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Temnopleuroidea; Toxopneustidae;
OC Lytechinus.
OX NCBI_TaxID=7654;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97333945; PubMed=9190067;
RT Kissinger J.C., Hahn J.H., Raff R.A.;
RT "Rapid evolution in a conserved gene family. Evolution of the actin
RT gene family in the sea urchin genus Helicidaris and related genera.";
RL Mol. Biol. Evol. 14:654-665(1997).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; U82544; AAB66301.1; -.
DR HSP; P10983; ID4X.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS 1; 1.
DR PROSITE; PS01132; ACTINS_ACT LIKE; 1.
KW Structural protein.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 12097 MW; F670D62101164AEA CRC64;
Query Match 100.0%; Score 82; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GRPRHQGVNMGQK 15
DB 23 GRPRHQGVNMGQK 37
Search completed: April 8, 2005, 12:03:06
Job time : 57.8667 secs

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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 62.4 Seconds
(without alignments)
92.971 Million cell updates/sec

Title: US-09-423-351C-4
Perfect score: 81
Sequence: 1 GGTMYPGIADRMQX 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	15	2	AAW92530 Beta-acti
2	81	100.0	86	4	ABG08617 Novel hum
3	81	100.0	100	4	AAW81404 Human hae
4	81	100.0	100	4	AAW81907 Human hae
5	81	100.0	110	5	ABP42328 Human ova
6	81	100.0	118	4	AU30705 Novel hum
7	81	100.0	145	5	ABP43127 Human ova
8	81	100.0	147	4	AAW80875 Human hae
9	81	100.0	147	4	AAW81886 Human hae
10	81	100.0	147	4	AAW81332 Human hae
11	81	100.0	148	3	AAW59047 Breast an
12	81	100.0	149	8	ABO84771 Human can
13	81	100.0	196	6	ABU70816 Human adi
14	81	100.0	214	8	ADR09052 Human pro
15	81	100.0	258	4	ABG00383 Novel hum
16	81	100.0	274	6	ABU70549 Human adi
17	81	100.0	294	7	AD163068 Human apo
18	81	100.0	297	4	ABG15100 Novel hum
19	81	100.0	332	7	AD163011 Human apo
20	81	100.0	334	6	ABP98860 Human str
21	81	100.0	342	7	ADM05323 Human pro
22	81	100.0	374	3	AAW78101 Misgurnus
23	81	100.0	374	3	AAW12985 Human bet
24	81	100.0	375	1	ABP61532 Sequence
25	81	100.0	375	2	AAW50328 Drug resi

26	81	100.0	375	2	AAW59176
27	81	100.0	375	3	AAW15017
28	81	100.0	375	3	AAW94569
29	81	100.0	375	5	ABW77395
30	81	100.0	375	6	ABW64271
31	81	100.0	375	6	ABW62328
32	81	100.0	375	6	ABW04830
33	81	100.0	375	7	ABW85212
34	81	100.0	375	7	ADW61174
35	81	100.0	375	7	ADP30525
36	81	100.0	375	7	AD163062
37	81	100.0	375	7	AD162970
38	81	100.0	375	7	AD163040
39	81	100.0	375	8	ADL13002
40	81	100.0	375	8	ADJ78489
41	81	100.0	375	8	ADL14103
42	81	100.0	375	8	ADP12391
43	81	100.0	375	8	ADQ26098
44	81	100.0	375	8	ABO84772
45	81	100.0	375	8	ABW80841

ALIGNMENTS

RESULT 1
AAW92530
ID AAW92530 standard; peptide; 15 AA.
XX AC AAW92530;
XX XX
DT 26-APR-1999 (first entry)
XX XX
DE Beta-actin reference peptide substrate #4.
XX XX
KW Peptide substrate; CCT; eukaryotic type II chaperonin complex; cyclin;
KW binding agent; substrate-binding site; SBS; substrate folding; actin;
KW tubulin; treatment; cancer; anticancer drug; viral infection; screening;
KW reduced toxicity.
XX XX
OS Synthetic.
XX XX
PN WO9853322-A1.
XX XX
PD 26-NOV-1998.
XX XX
PF 22-MAY-1998; 98WO-GB001485.
XX XX
PR 23-MAY-1997; 97GB-00010762.
XX XX
PA (CANC-) INST CANCER RES ROYAL CANCER HOSPITAL.
XX XX
PI Willison K, Hynes G, Liou AK;
XX WPI; 1999-070162/06.
XX XX
PT Identifying specific binding agents for substrate binding site in CCT
PT chaperonin complex; also new peptide binding agents and their mimetics,
PT and peptides containing a specific CCT binding site, used for treating
cancer.
XX XX
PS Disclosure; Fig 10; 97pp; English.
XX XX
CC This invention describes a method which uses the CCT (eukaryotic type II
CC chaperonin) complex or part of it, for identifying a binding agent that
CC can occupy a substrate-binding site (SBS) on the CCT complex. By binding
CC to the CCT complex, the binding agents block an SBS so that biological
CC activity of the CCT complex is affected, particularly its ability to fold
CC substrates such as actin, tubulin and cyclin. The binding agents are
CC useful for treatment of cancer, particularly when used in combination
CC with an anticancer drug, or viral infections. Nucleic acid fragments are
CC used to screen for agents, e.g. binding agents that modulate interaction
CC between the CCT complex and a protein that is to be folded. The binding

CC agents may target cells that are actively synthesising tubulin etc.
CC (unlike known microtubule-stabilising agents that affect all cells), so
CC should have reduced toxicity for normal cells. AAW92527-W92541 are
CC peptide substrates used in the method of the invention
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 81; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTMYPGIADRMQK 15
| | | | | | | | | | | | | | |
Db 1 GGTMYPGIADRMQK 15

RESULT 2
ID ABG08617 standard; protein; 86 AA.
XX
AC ABG08617;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #8608.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS72804.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 38976; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in

CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 86 AA;

Query Match 100.0%; Score 81; DB 4; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTMYPGIADRMQK 15
| | | | | | | | | | | | | | |
Db 12 GGTMYPGIADRMQK 26

RESULT 3
ID AAM81404 standard; protein; 100 AA.
XX
AC AAM81404;
XX
DT 13-NOV-2001 (first entry)
XX
DE Human haematological malignancy-related antigen #1102.
XX
KW Human; cytostatic; vascular; gene therapy; vaccine; lymphoma;
KW haematological malignancy; antigen; chronic lymphocytic leukaemia;
KW follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.
XX
OS Homo sapiens.
XX
PN WO200164886-A2.
XX
PD 07-SEP-2001.
XX
PF 01-MAR-2001; 2001WO-US007272.
XX
PR 01-MAR-2000; 2000US-0186126P.
PR 17-MAR-2000; 2000US-0190479P.
PR 27-APR-2000; 2000US-0200545P.
PR 28-APR-2000; 2000US-0200303P.
PR 28-APR-2000; 2000US-0200779P.
PR 01-MAY-2000; 2000US-0200999P.
PR 04-MAY-2000; 2000US-0202084P.
PR 22-MAY-2000; 2000US-0206201P.
PR 14-JUL-2000; 2000US-0218950P.
PR 03-AUG-2000; 2000US-0222903P.
PR 04-AUG-2000; 2000US-0223416P.
PR 07-AUG-2000; 2000US-0223378P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Gaiger A, Algate PA, Mannion J;
XX
DR WPI; 2001-514842/56.
XX
PT Compositions and methods for the detection of hematological malignancies,
PT e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and
PT Hodgkin's and T/B cell non-Hodgkin's lymphoma.
XX
PS Claim 1; Page 953; 1252pp; English.
XX
CC The present invention relates to compositions and methods for the
CC detection, diagnosis and therapy of haematological malignancies. The
CC present sequence is the protein sequence of a human haematological
CC malignancy related antigen. The methods of the present invention comprise
CC detecting the presence of haematological malignancy related antigen(s) in
CC a sample obtained from the patient (an increased level of the
CC polypeptide, compared to an unaffected individual, is indicative of an
CC increased risk). Haematological malignancies which can be treated using
CC the present invention are chronic lymphocytic leukaemia, lymphoma,
CC follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B
CC cell non-Hodgkin's lymphoma
XX

```

SQ Sequence 100 AA;
Query Match      100.0%; Score 81; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTMYPGIADRMQK 15
   |||||
DB 46 GGTMYPGIADRMQK 60

RESULT 5
AAM81907
ID AAM81907 standard; protein; 100 AA.
XX AC AAM81907;
XX DT 13-NOV-2001 (first entry)
XX DE Human haematological malignancy-related antigen #1605.
XX KW Human; cytostatic; vascular; gene therapy; vaccine; lymphoma;
KW haematological malignancy; antigen; chronic lymphocytic leukaemia;
KW follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.
XX OS Homo sapiens.
XX PN WO200164886-A2.
XX PD 07-SEP-2001.
XX PF 01-MAR-2001; 2001WO-US007272.
XX PR 01-MAR-2000; 2000US-0186126P.
XX PR 17-MAR-2000; 2000US-0190479P.
XX PR 27-APR-2000; 2000US-0200545P.
XX PR 28-APR-2000; 2000US-0200303P.
XX PR 28-APR-2000; 2000US-0200779P.
XX PR 01-MAY-2000; 2000US-0200999P.
XX PR 04-MAY-2000; 2000US-0202084P.
XX PR 22-MAY-2000; 2000US-0206201P.
XX PR 14-JUL-2000; 2000US-0218950P.
XX PR 03-AUG-2000; 2000US-0222903P.
XX PR 04-AUG-2000; 2000US-0223416P.
XX PR 07-AUG-2000; 2000US-0223378P.
XX PA (CORI-) CORIXA CORP.
XX PI Gaiger A, Algate PA, Mannion J;
XX DR WPI; 2001-514842/56.
XX PS Claim 1; Page 1149-1150; 1252pp; English.
XX CC The present invention relates to compositions and methods for the
CC detection, diagnosis and therapy of haematological malignancies. The
CC present sequence is the protein sequence of a human haematological
CC malignancy related antigen. The methods of the present invention comprise
CC detecting the presence of haematological malignancy related antigen(s) in
CC a sample obtained from the patient (an increased level of the
CC polypeptide, compared to an unaffected individual, is indicative of an
CC increased risk). Haematological malignancies which can be treated using
CC the present invention are chronic lymphocytic leukaemia, lymphoma,
CC follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B
CC cell non-Hodgkin's lymphoma
XX SQ Sequence 100 AA;
Query Match      100.0%; Score 81; DB 4; Length 100;

Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTMYPGIADRMQK 15
   |||||
DB 46 GGTMYPGIADRMQK 60

RESULT 5
ABP42928
ID ABP42928 standard; protein; 110 AA.
XX AC ABP42928;
XX DT 22-AUG-2002 (first entry)
XX DE Human ovarian antigen HPRDS46, SEQ ID NO:4060.
XX KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive.
XX OS Homo sapiens.
XX PN WO200200677-A1.
XX PD 03-JAN-2002.
XX PF 07-JUN-2001; 2001WO-US018569.
XX PR 07-JUN-2000; 2000US-0209467P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Birse CE, Rosen CA;
XX DR WPI; 2002-147878/19.
XX DR N-PSDB; ABQ56005.
XX PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
XX useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
XX cancer), immune disorders, cardiovascular disorders and neurological
XX diseases.
XX PS Claim 11; SEQ ID NO 4060; 2922pp; English.
XX CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
XX ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
XX encompasses polypeptides 90% identical and polynucleotides 95% identical
XX to the sequences of the invention. The invention additionally relates to
XX recombinant vectors and host cells comprising human ovarian antigen
XX polynucleotides, antibodies against human ovarian antigens, and the use
XX of ovarian antigen polynucleotides and polypeptides in diagnosing,
XX treating, prognosing or preventing various ovary and/or breast-related
XX disorders. Such conditions include ovarian cancer and breast cancer, and
XX metastatic tumours of ovarian or breast origin, reproductive system
XX disorders (e.g., infertility, disorders of pregnancy, anovulation,
XX polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
XX disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
XX shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
XX vaginitis), immune disorders (e.g., congenital and acquired
XX immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
XX blood-related disorders (e.g., anaemia), cardiovascular disorders,
XX respiratory disorders, neurological disorders, gastrointestinal disorders
XX and urinary system disorders. Ovarian antigen polypeptides and
XX polynucleotides may also be used in screening for compounds which

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CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a human ovarian antigen of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 110 AA;

Query Match 100.0%; Score 81; DB 5; Length 110;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTMYPGIADRMQK 15
Db 36 GGTMYPGIADRMQK 50
|||||

RESULT 6
AAU30705
ID AAU30705 standard; protein; 118 AA.
XX
AC AAU30705;
DT 18-DEC-2001 (first entry)
XX
DE Novel human secreted protein #1196.
XX
KW Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
OS Homo sapiens.
XX
XX WO200179449-A2.
XX
XX 25-OCT-2001.
XX
XX 16-APR-2001; 2001WO-US008656.
XX
XX 18-APR-2000; 2000US-00552929.
XX
XX 26-JAN-2001; 2001US-00770160.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-611725/70.
XX
XX Nucleic acids encoding a range of human polypeptides, useful in genetic
XX vaccination, testing and therapy.
XX
XX
PS Claim 20; Page 333; 765pp; English.
XX
XX The invention relates to novel human secreted polypeptides. The
XX polypeptides and antibodies to the polypeptides are useful for
XX determining the presence of or predisposition to a disease associated
XX with altered levels of polypeptide. The polypeptides are also useful for
XX identifying agents (agonists and antagonists) that bind to them. Cells
XX expressing the proteins are useful for identifying a therapeutic agent
XX for use in treatment of a pathology related to aberrant expression or
XX physiological interactions of the polypeptide. Vectors comprising the
XX nucleic acids encoding the polypeptides and cells genetically engineered
XX to express them are also useful for producing the proteins. The proteins
XX are useful in genetic vaccination, testing and therapy, and can be used
XX as nutritional supplements. They may be used to increase stem cell
XX proliferation, to regulate haematopoiesis; and in bone, cartilage, tendon
XX and/or nerve tissue growth or regeneration; immune suppression and/or
XX stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
XX AAU29510-AAU33304 represent the amino acid sequences of novel human

CC secreted proteins of the invention
XX
XX Sequence 118 AA;

Query Match 100.0%; Score 81; DB 4; Length 118;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTMYPGIADRMQK 15
Db 42 GGTMYPGIADRMQK 56
|||||

RESULT 7
ABP43127
ID ABP43127 standard; protein; 145 AA.
XX
AC ABP43127;
XX
XX 22-AUG-2002 (first entry)
XX
XX Human ovarian antigen HVBD91, SEQ ID NO:4259.
XX
XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive.
XX
XX Homo sapiens.
OS
XX
XX WO200200677-A1.
XX
XX 03-JAN-2002.
XX
XX 07-JUN-2001; 2001WO-US018569.
XX
XX 07-JUN-2000; 2000US-0209467P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Birse CE, Rosen CA;
XX
XX WPI; 2002-147878/19.
XX
XX N-PSDB; ABQ56204.
XX
XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
XX useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
XX cancer), immune disorders, cardiovascular disorders and neurological
XX diseases.
XX
XX Claim 11; SEQ ID NO 4259; 2922pp; English.
XX
XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
XX ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
XX encompasses polypeptides 90% identical and polynucleotides 95% identical
XX to the sequences of the invention. The invention additionally relates to
XX recombinant vectors and host cells comprising human ovarian antigen
XX polynucleotides, antibodies against human ovarian antigens, and the use
XX of ovarian antigen polynucleotides and polypeptides in diagnosing,
XX treating, prognosing or preventing various ovary and/or breast-related
XX disorders. Such conditions include ovarian cancer and breast cancer, and
XX metastatic tumours of ovarian or breast origin, reproductive system
XX disorders (e.g., infertility, disorders of pregnancy, anovulation
XX polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
XX disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
XX shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
XX vaginitis), immune disorders (e.g., congenital and acquired

CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 145 AA;

Query Match 100.0%; Score 81; DB 5; Length 145;
 Best Local Similarity 100.0%; Pred. No. 3.9e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTMYPGIADRMQK 15
 |||||
 DB 71 GGTMYPGIADRMQK 85

RESULT 8
 AAM80875
 ID AAM80875 standard; protein; 147 AA.
 XX
 AC AAM80875;
 XX
 DT 13-NOV-2001 (first entry)
 XX
 DE Human haematological malignancy-related antigen #573.
 XX
 KW Human; cytostatic; vascular; gene therapy; vaccine; lymphoma;
 KW haematological malignancy; antigen; chronic lymphocytic leukaemia;
 KW follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.
 XX
 OS Homo sapiens.

XX WO200164886-A2.
 XX PD 07-SEP-2001.
 XX PF 01-MAR-2001; 2001WO-US007272.
 XX PR 01-MAR-2000; 2000US-0186126P.
 XX PR 17-MAR-2000; 2000US-0190479P.
 XX PR 27-APR-2000; 2000US-0200545P.
 XX PR 28-APR-2000; 2000US-0200303P.
 XX PR 01-MAY-2000; 2000US-0200999P.
 XX PR 04-MAY-2000; 2000US-0202084P.
 XX PR 22-MAY-2000; 2000US-0206201P.
 XX PR 03-AUG-2000; 2000US-0222903P.
 XX PR 07-AUG-2000; 2000US-0223378P.
 XX
 XX (CORI-) CORIXA CORP.
 XX
 XX Gaiger A, Algate PA, Mannion J;
 XX WPI; 2001-514842/56.
 XX
 XX Compositions and methods for the detection of hematological malignancies,
 PT e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and
 PT Hodgkin's and T/B cell non-Hodgkin's lymphoma.
 XX
 PS Claim 1; Page 743-744; 1252pp; English.

CC The present invention relates to compositions and methods for the
 CC detection, diagnosis and therapy of haematological malignancies. The
 CC present sequence is the protein sequence of a human haematological
 CC malignancy related antigen. The methods of the present invention comprise
 CC detecting the presence of haematological malignancy related antigen(s) in
 CC a sample obtained from the patient (an increased level of the
 CC polypeptide, compared to an unaffected individual, is indicative of an
 CC increased risk). Haematological malignancies which can be treated using
 CC the present invention are chronic lymphocytic leukaemia, lymphoma,
 CC follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B
 CC cell non-Hodgkin's lymphoma
 XX
 SQ Sequence 147 AA;

Query Match 100.0%; Score 81; DB 4; Length 147;
 Best Local Similarity 100.0%; Pred. No. 4e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTMYPGIADRMQK 15
 |||||
 DB 73 GGTMYPGIADRMQK 87

RESULT 9
 AAM81886
 ID AAM81886 standard; protein; 147 AA.
 XX
 AC AAM81886;
 XX
 DT 13-NOV-2001 (first entry)
 XX
 DE Human haematological malignancy-related antigen #1584.
 XX
 KW Human; cytostatic; vascular; gene therapy; vaccine; lymphoma;
 KW haematological malignancy; antigen; chronic lymphocytic leukaemia;
 KW follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.
 XX
 OS Homo sapiens.

XX WO200164886-A2.
 XX PD 07-SEP-2001.
 XX PF 01-MAR-2001; 2001WO-US007272.
 XX PR 01-MAR-2000; 2000US-0186126P.
 XX PR 17-MAR-2000; 2000US-0190479P.
 XX PR 27-APR-2000; 2000US-0200545P.
 XX PR 28-APR-2000; 2000US-0200303P.
 XX PR 01-MAY-2000; 2000US-0200779P.
 XX PR 04-MAY-2000; 2000US-0202084P.
 XX PR 22-MAY-2000; 2000US-0206201P.
 XX PR 14-JUL-2000; 2000US-0218950P.
 XX PR 03-AUG-2000; 2000US-0222903P.
 XX PR 04-AUG-2000; 2000US-0223416P.
 XX PR 07-AUG-2000; 2000US-0223378P.
 XX
 XX (CORI-) CORIXA CORP.
 XX
 XX Gaiger A, Algate PA, Mannion J;
 XX WPI; 2001-514842/56.
 XX
 XX Compositions and methods for the detection of hematological malignancies,
 PT e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and
 PT Hodgkin's and T/B cell non-Hodgkin's lymphoma.
 XX
 PS Claim 1; Page 1141; 1252pp; English.

XX The present invention relates to compositions and methods for the
 CC detection, diagnosis and therapy of haematological malignancies. The
 CC present sequence is the protein sequence of a human haematological

CC malignancy related antigen. The methods of the present invention comprise
CC detecting the presence of haematological malignancy related antigen(s) in
CC a sample obtained from the patient (an increased level of the
CC polypeptide, compared to an unaffected individual, is indicative of an
CC increased risk). Haematological malignancies which can be treated using
CC the present invention are chronic lymphocytic leukaemia, lymphoma,
CC follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B
CC cell non-Hodgkin's lymphoma

XX Sequence 147 AA;

Query Match 100.0%; Score 81; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTWYPGIADRMQK 15
|||||
DB 73 GGTWYPGIADRMQK 87

RESULT 10

AA81332
ID AA81332 standard; protein; 147 AA.

AC AA81332;

DT 13-NOV-2001 (first entry)

XX Human haematological malignancy-related antigen #1030.

DE Human; cytostatic; vascular; gene therapy; vaccine; lymphoma;
XX haematological malignancy; antigen; chronic lymphocytic leukaemia;
KW follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.

XX Homo sapiens.

OS WO200164886-A2.

PN 07-SEP-2001.

PD 01-MAR-2001; 2001WO-US007272.

PF 01-MAR-2000; 2000US-0186126P.

PR 17-MAR-2000; 2000US-0190479P.

PR 27-APR-2000; 2000US-0200545P.

PR 28-APR-2000; 2000US-0200303P.

PR 28-APR-2000; 2000US-0200779P.

PR 01-MAY-2000; 2000US-0200999P.

PR 04-MAY-2000; 2000US-0202084P.

PR 14-JUL-2000; 2000US-0218950P.

PR 03-AUG-2000; 2000US-0222903P.

PR 04-AUG-2000; 2000US-0223416P.

PR 07-AUG-2000; 2000US-0223378P.

XX (CORI-) CORIXA CORP.

XX Gaiger A, Algate PA, Mannion J;

XX WPI; 2001-514842/56.

XX Compositions and methods for the detection of hematological malignancies,

XX e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and

XX Hodgkin's and T/B cell non-Hodgkin's lymphoma.

XX Claim 1; Page 925; 1252pp; English.

XX The present invention relates to compositions and methods for the

XX detection, diagnosis and therapy of haematological malignancies. The

XX present sequence is the protein sequence of a human haematological

XX malignancy related antigen. The methods of the present invention comprise

CC polypeptide, compared to an unaffected individual, is indicative of an
CC increased risk). Haematological malignancies which can be treated using
CC the present invention are chronic lymphocytic leukaemia, lymphoma,
CC follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B
CC cell non-Hodgkin's lymphoma

XX Sequence 147 AA;

Query Match 100.0%; Score 81; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTWYPGIADRMQK 15
|||||
DB 73 GGTWYPGIADRMQK 87

RESULT 11

AA859047
ID AA859047 standard; protein; 148 AA.

AC AA859047;

XX 27-MAR-2001 (first entry)

XX Breast and ovarian cancer associated antigen protein sequence SEQ ID 755.

DE Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
XX neurotropic; neuroprotective; antiviral; antiallergic; hepatotropic;
KW antidiabetic; antiinflammatory; antitumor; antitumor; antitumor;
KW antibacterial; antifungal; antiparasitic; cardiac; immune disorder;
KW Addison's disease; allergy; autoimmune haemolytic anaemia;
KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
KW cardiovascular disorder; wound healing; neurological disease.

XX Homo sapiens.

OS WO200055173-A1.

PN 21-SEP-2000.

PD 08-MAR-2000; 2000WO-US005881.

PR 12-MAR-1999; 99US-0124270P.

PR (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI; 2000-611515/58.

XX N-PSDB; AAF21950.

XX New human breast and ovarian cancer associated gene sequences and the
XX polypeptides encoded by these genes, useful in the prevention, treatment
XX and diagnosis of cancer, immune disorders, cardiovascular disorders and
XX neurological diseases.

XX Claim 11; Page 1223; 1299pp; English.

XX Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
XX proteins AAB58711 - AAB59128. The DNA and protein sequences are
XX associated with breast and ovarian cancer. Included in the invention are
XX sequences AAF22032 - AAF22040 and AAB59129 which are used in the
XX isolation and characterisation of the DNA and protein sequences of the
XX invention. The breast and ovarian cancer associated DNA, protein, agonist
XX or antagonist sequences exhibit cytostatic; immunosuppressive; neurotropic;
XX neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic;
XX antiinflammatory; antitumor; antitumor; antitumor; antitumor;
XX antifungal; antiparasitic and cardiac activity. The polynucleotide and
XX protein sequences are used in the diagnosis of cancer, particularly
XX breast and ovarian cancer. The nucleic acid sequences, proteins, agonists
XX and antagonists may also be used in the diagnosis, prevention and treatment

CC of immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
 CC cardiovascular disorders such as myocardial ischaemias; wound healing;
 CC neurological diseases such as cerebral anoxia and epilepsy; and
 CC infectious diseases
 XX
 SQ Sequence 148 AA;

Query Match 100.0%; Score 81; DB 3; Length 148;
 Best Local Similarity 100.0%; Pred. No. 4e-06; Mismatches 0; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTWYPGIADRMOK 15
 |||||
 DB 19 GGTWYPGIADRMOK 33

RESULT 12
 ABO84771
 ID ABO84771 standard; protein; 149 AA.
 XX
 AC ABO84771;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human cancer-associated protein (CAP) HP07-010.
 XX
 KW Human; cancer-associated protein; CAP; cancer; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO2004058146-A2.
 XX
 PD 15-JUL-2004.
 XX
 PF 15-DEC-2003; 2003WO-US040081.
 XX
 PR 17-DEC-2002; 2002US-00322281.
 XX
 PA (SAGR-) SAGRES DISCOVERY INC.
 XX
 PI Morris DW, Malandro MS;
 XX
 DR WPI; 2004-499109/47.
 DR N-PSDB; ABO33111.
 XX

Novel human cancer associated protein encoded within open reading frame
 of cancer associated gene, useful as targets for diagnosing cancer.

Claim 18; SEQ ID NO 66; 182pp; English.

The invention relates to cancer-associated proteins (CAP) and the cancer-associated (CA) nucleic acids encoding them. The invention also relates to a method for treating cancers involving administering to a patient an inhibitor of CAP, and a method of screening for anticancer activity in a potential drug involving providing a cell that expresses a CA gene, contacting a tissue sample derived from a cancer cell with an anticancer drug candidate and monitoring the effect of the anticancer drug candidate on expression of the CA gene. The CAP proteins are useful for detecting cancer associated with expression of a CAP protein in a test cell sample and for screening for a bioactive agent capable of modulating the activity of a CAP protein. The CA nucleic acids are useful for diagnosing cancer, involving determining the expression of a CA nucleic acid in a tissue. This sequence represents a human CAP of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Query Match 100.0%; Score 81; DB 8; Length 149;
 Best Local Similarity 100.0%; Pred. No. 4e-06;

Sequence 149 AA;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTWYPGIADRMOK 15
 |||||
 DB 75 GGTWYPGIADRMOK 89

RESULT 13
 ABU70816
 ID ABU70816 standard; protein; 196 AA.
 XX
 AC ABU70816;
 XX
 DT 10-JUN-2003 (first entry)
 XX
 DE Human adipocyte Selected Interacting domain, SID, #447.

Human; prey; adipocyte; SID; selected interacting domain; anorectic;
 antidiabetic; protein-protein interaction; diabetes;
 yeast 2-hybrid assay; metabolic disorder; obesity.

OS Homo sapiens.
 XX
 PN WO200286122-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 14-MAR-2002; 2002WO-EP003768.
 XX
 PR 14-MAR-2001; 2001US-0275734P.
 XX
 PA (HYBR-) HYBRIGENICS.
 XX
 PI Legrain P, Daviet L;
 XX
 DR WPI; 2003-103412/09.
 DR N-PSDB; ACAS7360.
 XX

New complex between two interacting proteins in adipocyte cells, useful for identifying selected interacting domains that modulate protein interactions, or for preventing or treating metabolic disorders such as obesity or diabetes.

Claim 6; Page 259-260; 382pp; English.

The invention relates to a complex between two interacting proteins in adipocyte cells, given in the specification. The proteins are identified by selecting a bait protein from a known adipocyte marker and then performing a yeast 2-hybrid selection to isolate prey proteins encoded by members of an adipocyte cDNA library. The proteins are designated SID (RTM) (selected interacting domains) proteins. Also included are a polynucleotide encoding a polypeptide in the adipocyte cells, a recombinant host cell expressing at least one of the interacting polypeptides of the complex, selecting a modulating compound in adipocyte cells, a SID (RTM) polypeptide comprising any of the 738 amino acid sequences given in the specification (including its fragment or variant), a SID (RTM) polynucleotide comprising any of the 738 nucleotide sequences given in the specification (including its fragment or variant), a vector comprising the SID (RTM) polynucleotide, a recombinant host cell comprising the vector, a protein chip comprising the polypeptides and a record comprising all or part of the data, listed in the specification. The complex, polypeptides, polynucleotides and compounds are useful for preventing or treating metabolic disorders such as obesity or diabetes. The polynucleotides are useful as probes or primers. The complex is particularly useful for identifying selected interacting domains (SID (RTM)) for screening drugs that modulate the protein interaction, thus exhibiting the therapeutic effect. The present sequence represents a SID (prey) protein of the invention

Sequence 196 AA;

Query Match 100.0%; Score 81; DB 6; Length 196;
 Best Local Similarity 100.0%; Pred. No. 5.4e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTMPGADRMQK 15
| | | | | | | | | |
Db 175 GGTTMPGADRMQK 189

RESULT 14
ADR09052
ID ADR09052 standard; protein; 214 AA.

XX AC ADR09052;

XX DT 04-NOV-2004 (first entry)

XX DE Human protein useful for treating neurological disease Seq 2558.

XX KW human; oligo-capping method; diagnostic marker; gene therapy;

XX KW osteoporosis; neurological disease; Alzheimer's disease;

XX KW Parkinson's disease; dementia; short memory; cancer;

XX KW sense or motor function; emotional reaction; fear response; panic;

XX KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;

XX KW tranquiliser.

XX OS Homo sapiens.

XX XX EP1447413-A2.

XX FN 18-AUG-2004.

XX PD 12-FEB-2004; 2004EP-00003145.

XX PF 14-FEB-2003; 2003JP-00102207.

XX PR 09-MAY-2003; 2003JP-00131452.

XX XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX XX Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;

XX PI Wakamatsu A, Ishii S, Nagai K, Irie R;

XX DR WPI; 2004-583265/57.

XX DR N-PSDB; ADR07096.

XX PT New 1995 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.

XX PS Claim 1; SEQ ID NO 2558; 2686pp; English.

XX CC This invention relates to novel, isolated full length human cDNA

XX CC molecules and the encoded proteins thereof. Specifically, it refers to

XX CC cDNA clones obtained by an oligo-capping method, where none of these

XX CC clones are identical to any known human mRNAs. The present invention

XX CC describes an immunoassay to identify agonists and antagonists, as well as

XX CC antibodies, antisense molecules and siRNAs that can all be used to bind

XX CC to and modulate expression of the cDNA molecules. As such, these

XX CC molecules are useful for diagnostic markers or therapeutic targets for

XX CC the various diseases or morbid states. In particular, they are useful in

XX CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's

XX CC disease, Parkinson's disease, dementia, short memory and various cancers,

XX CC as well as for maintaining equilibrium of sense or motor function, and

XX CC for treating emotional reaction, fear response and panic. Accordingly,

XX CC they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,

XX CC cytostatic and tranquiliser activities. This polypeptide is a protein

XX CC encoded by a full length human cDNA sequence of the invention. NOTE: This

XX CC sequence is not given in the sequence listing of the specification but

XX CC can be obtained on CD-ROM from the European Patent Office, Vienna Sub-

XX CC office.

XX SQ Sequence 214 AA;

Query Match 100.0%; Score 81; DB 8; Length 214;

Best Local Similarity 100.0%; Pred. No. 5.9e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTMPGADRMQK 15
| | | | | | | | | |
Db 157 GGTTMPGADRMQK 171

RESULT 15
ABG00383
ID ABG00383 standard; protein; 258 AA.

XX AC ABG00383;

XX DT 13-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #374.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS64570.

XX PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX PS Claim 20; SEQ ID NO 30742; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological actions in
CC polynucleotide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG03077 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 258 AA;

Query Match 100.0%; Score 81; DB 4; Length 258;

Best Local Similarity 100.0%; Pred. No. 7.2e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTMPGADRMQK 15

Db 192 GGTMYPGIADRMQK 206
|||||

Search completed: April 8, 2005, 10:50:43
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OM protein - protein search, using sw model

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(without alignments)
63.863 Million cell updates/sec

Title: US-09-423-351C-4
Perfect score: 81
Sequence: 1 GGTMYPGIADRMQK 15

Scoring table: BLOSUM62
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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/iaa/ECTUS_COMB.pep: *
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	60	3	US-09-306-446C-6
2	81	100.0	239	4	US-09-949-016-10409
3	81	100.0	374	3	US-08-609-236-6
4	81	100.0	374	3	US-09-306-446C-2
5	81	100.0	375	3	US-09-106-217-16
6	81	100.0	375	4	US-09-976-594-731
7	81	100.0	376	1	US-08-588-113-2
8	81	100.0	376	4	US-09-949-016-6100
9	81	100.0	377	3	US-09-106-217-2
10	81	100.0	377	4	US-09-919-172-33
11	81	100.0	377	4	US-09-917-254-53
12	81	100.0	386	4	US-09-949-016-7721
13	81	100.0	399	4	US-09-949-016-9424
14	81	100.0	402	4	US-09-949-016-10757
15	81	100.0	404	4	US-09-949-016-11313
16	78	96.3	375	3	US-09-171-337A-7
17	78	96.3	375	3	US-09-631-022-7
18	76	93.8	375	3	US-09-171-337A-8
19	76	93.8	375	4	US-09-631-022-8
20	73	90.1	375	2	US-08-494-151-14
21	73	90.1	377	4	US-09-248-796A-14109
22	66	81.5	21	3	US-08-936-477-1
23	66	81.5	21	4	US-09-786-066-16
24	66	81.5	21	5	PCT-US94-10051-1
25	55	67.9	21	4	US-09-786-066-2
26	55	67.9	21	4	US-09-786-066-9
27	55	67.9	394	4	US-09-949-016-6655

28	55	67.9	406	4	US-09-949-016-7396	Sequence 7396, Ap
29	54	66.7	129	4	US-09-248-796A-14107	Sequence 14107, A
30	43	53.1	471	4	US-09-583-110-3667	Sequence 3667, Ap
31	43	53.1	471	4	US-08-378-213-2	Sequence 2, Appli
32	43	53.1	471	4	US-08-378-213-4	Sequence 4, Appli
33	43	53.1	471	4	US-08-378-213-5	Sequence 5, Appli
34	43	53.1	471	4	US-09-120-044-3	Sequence 3, Appli
35	43	53.1	471	4	US-09-120-044-4	Sequence 4, Appli
36	43	53.1	472	4	US-09-107-433-3566	Sequence 3566, Ap
37	43	53.1	533	4	US-09-902-540-14623	Sequence 14623, A
38	42	51.9	347	4	US-09-543-681A-8255	Sequence 8255, Ap
39	41	50.6	340	4	US-09-214-631-3	Sequence 3, Appli
40	41	50.6	340	4	US-09-051-994-2	Sequence 2, Appli
41	41	50.6	340	4	US-08-635-130A-4	Sequence 4, Appli
42	41	50.6	340	4	US-09-949-016-6076	Sequence 6076, Ap
43	41	50.6	362	4	US-09-949-016-7725	Sequence 7725, Ap
44	41	50.6	376	4	US-09-538-092-1109	Sequence 1109, Ap
45	41	50.6	376	4	US-09-538-092-1110	Sequence 1110, Ap

ALIGNMENTS

RESULT 1
US-09-306-446C-6
; Sequence 6, Application US/09306446C
; Patent No. 6372959
; GENERAL INFORMATION:
; APPLICANT: KIM, Dong Soo
; APPLICANT: KIM, Chul Geun
; APPLICANT: NAM, Yoon Kwon
; APPLICANT: NOH, Jae Koo
; APPLICANT: CHO, Kyoun Nam
; TITLE OF INVENTION: EXPRESSION VECTOR OF MUD LOACH GROWTH HORMONE GENE
; FILE REFERENCE: P06344050/BAS
; CURRENT APPLICATION NUMBER: US/09/306.446C
; CURRENT FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: KR 98/20255
; PRIOR FILING DATE: 1998-06-01
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Misgurnus mizolepus
US-09-306-446C-6

Query Match 100.0%; Score 81; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTMYPGIADRMQK 15
Db 33 GGTMYPGIADRMQK 47

RESULT 2
US-09-949-016-10409
; Sequence 10409, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO001307
; CURRENT APPLICATION NUMBER: US/09/949.016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 10409
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10409

Query Match 100.0%; Score 81; DB 4; Length 239;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTMYPGIADRMQK 15
|||||
DB 165 GGTMYPGIADRMQK 179

RESULT 3
US-08-609-236-6
; Sequence 6, Application US/08609236
; Patent No. 6087398
; GENERAL INFORMATION:
; APPLICANT: Steven R. Goodman
; TITLE OF INVENTION: No. 6087398el sickle Cell Anemia Treatment
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McGregor & Adler, LLP
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,236
; FILING DATE: March 1, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/002,288
; FILING DATE: August 14, 1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Benjamin Aaron Adler, Ph.D.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5807
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6908
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374
; TYPE: Amino acid
; STRANDEDNESS:
; TOPOLOGY: Linear
; MOLECULE TYPE:
; DESCRIPTION: Protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:

US-08-609-236-6 Query Match 100.0%; Score 81; DB 3; Length 374;

Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTMYPGIADRMQK 15
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DB 300 GGTMYPGIADRMQK 314

RESULT 4
US-09-306-446C-2
; Sequence 2, Application US/09306446C
; Patent No. 6372959
; GENERAL INFORMATION:
; APPLICANT: KIM, Dong Soo
; APPLICANT: KIM, Chul Geun
; APPLICANT: NAM, Yoon Kwon
; APPLICANT: NOH, Jae Koo
; APPLICANT: CHO, Kyou Nam
; TITLE OF INVENTION: EXPRESSION VECTOR OF MUD LOACH GROWTH HORMONE GENE
; FILE REFERENCE: P06344US0/BAS
; CURRENT APPLICATION NUMBER: US/09/306,446C
; CURRENT FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: KR 98/20255
; PRIOR FILING DATE: 1998-06-01
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Misgurnus mizolepus
US-09-306-446C-2

Query Match 100.0%; Score 81; DB 3; Length 374;
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTMYPGIADRMQK 15
|||||
DB 300 GGTMYPGIADRMQK 314

RESULT 5
US-09-106-217-16
; Sequence 16, Application US/09106217
; Patent No. 6063576
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Olson, Timothy M.
; TITLE OF INVENTION: Actin Mutations in Dilated
; TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; STREET: Tower
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,217
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 36,609
; REFERENCE/DOCKET NUMBER: 2323-125
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-783-6040
TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-106-217-16

Query Match 100.0%; Score 81; DB 3; Length 375;
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTWYPGIADRMQK 15
|||||
DB 301 GGTWYPGIADRMQK 315

RESULT 6

US-09-594-594-731
Sequence 731, Application US/09976594
Patent No. 6673549

GENERAL INFORMATION:

APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
SEQ ID NO 731
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6673549 1837317CDD1
US-09-594-594-731

Query Match 100.0%; Score 81; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTWYPGIADRMQK 15
|||||
DB 301 GGTWYPGIADRMQK 315

RESULT 7

US-08-588-113-2
Sequence 2, Application US/08588113
Patent No. 5710003

GENERAL INFORMATION:

APPLICANT: McHugh, Kirk M.
TITLE OF INVENTION: DIAGNOSTIC TEST FOR DETERMINING
TITLE OF INVENTION: MALIGNANCY OF SMOOTH MUSCLE TUMORS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 57100318
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,113
FILING DATE:

CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:
NAME: Ralph, Rebecca L.
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: TJU-1652
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-588-113-2

Query Match 100.0%; Score 81; DB 1; Length 376;
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTWYPGIADRMQK 15
|||||
DB 302 GGTWYPGIADRMQK 316

RESULT 8

US-09-949-016-6100
Sequence 6100, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6100
LENGTH: 376
TYPE: PRT
ORGANISM: Human
US-09-949-016-6100

Query Match 100.0%; Score 81; DB 4; Length 376;
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTWYPGIADRMQK 15
|||||
DB 302 GGTWYPGIADRMQK 316

RESULT 9

US-09-106-217-2
Sequence 2, Application US/09106217
Patent No. 6063576
GENERAL INFORMATION:

APPLICANT: Keating, Mark T.
APPLICANT: Olson, Timothy M.
TITLE OF INVENTION: Actin Mutations in Dilated
TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
NUMBER OF SEQUENCES: 18

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
;; STREET: 555 Thirteenth Street, N.W., Suite 701 East
;; STREET: Tower
;; CITY: Washington
;; STATE: DC
;; COUNTRY: U.S.A.
;; ZIP: 20004
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/106,217
;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Saxe, Stephen A.
;; REGISTRATION NUMBER: 38,609
;; REFERENCE/DOCKET NUMBER: 2323-125
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-783-6040
;; TELEFAX: 202-783-6031
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 377 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-106-217-2

Query Match 100.0%; Score 81; DB 3; Length 377;
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTMYPGIADRMOK 15
|||
Db 303 GGTTMYPGIADRMOK 317

RESULT 10
US-09-919-172-33
; Sequence 33, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Paris, Mary
; TITLE OF INVENTION: TURNER, Christopher M.
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 33
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 1709118CD1
US-09-919-172-33

Query Match 100.0%; Score 81; DB 4; Length 377;
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTMYPGIADRMOK 15
|||
Db 303 GGTTMYPGIADRMOK 317

RESULT 11
US-09-917-254-53
; Sequence 53, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
; APPLICANT: Mutter, George
; APPLICANT: Baak, Jan
; TITLE OF INVENTION: Prognostic Classification of Breast Cancer
; FILE REFERENCE: B0801/7224(JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/222,093
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 53
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-917-254-53

Query Match 100.0%; Score 81; DB 4; Length 377;
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTMYPGIADRMOK 15
|||
Db 303 GGTTMYPGIADRMOK 317

RESULT 12

US-09-949-016-7721
; Sequence 7721, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7721
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7721

Query Match 100.0%; Score 81; DB 4; Length 386;
Best Local Similarity 100.0%; Pred. No. 4.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTMYPGIADRMOK 15
|||
Db 312 GGTTMYPGIADRMOK 326

RESULT 13

US-09-949-016-9424
; Sequence 9424, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7721
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9424

Query Match 100.0%; Score 81; DB 4; Length 386;
Best Local Similarity 100.0%; Pred. No. 4.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTMYPGIADRMOK 15
|||
Db 312 GGTTMYPGIADRMOK 326

; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9424
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9424

Query Match 100.0%; Score 81; DB 4; Length 399;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTMYPGIADRMQK 15
Db 325 GGTMYPGIADRMQK 339

RESULT 14

US-09-949-016-10757
; Sequence 10757, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10757
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10757

Query Match 100.0%; Score 81; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTMYPGIADRMQK 15
Db 328 GGTMYPGIADRMQK 342

RESULT 15

US-09-949-016-11313
; Sequence 11313, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11313
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11313

Query Match 100.0%; Score 81; DB 4; Length 404;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTMYPGIADRMQK 15
Db 330 GGTMYPGIADRMQK 344

Search completed: April 8, 2005, 12:07:35
Job time : 18.5333 secs

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; PRIOR FILING DATE: 2000-08-07
 ; NUMBER OF SEQ ID NOS: 9597
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1768
 ; LENGTH: 100
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-796-692-1768

Query Match 100.0%; Score 81; DB 9; Length 100;
 Best Local Similarity 100.0%; Pred. No. 2.6e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTMPGFIADRMQK 15
 Db 46 GGTTMPGFIADRMQK 60

RESULT 2

US-09-796-692-2271
 ; Sequence 2271, Application US/09796692
 ; Publication No. US20020198362A1
 ; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Algate, Paul A.
 ; APPLICANT: Mannion, Jane
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
 ; FILE REFERENCE: 2077.001200
 ; CURRENT APPLICATION NUMBER: US/09/796,692
 ; PRIOR FILING DATE: 2001-03-01
 ; PRIOR APPLICATION NUMBER: 60/186,126
 ; PRIOR FILING DATE: 2000-03-01
 ; PRIOR APPLICATION NUMBER: 60/190,479
 ; PRIOR FILING DATE: 2000-03-17
 ; PRIOR APPLICATION NUMBER: 60/200,545
 ; PRIOR FILING DATE: 2000-04-27
 ; PRIOR APPLICATION NUMBER: 60/200,303
 ; PRIOR FILING DATE: 2000-04-28
 ; PRIOR APPLICATION NUMBER: 60/200,779
 ; PRIOR FILING DATE: 2000-04-28
 ; PRIOR APPLICATION NUMBER: 60/200,999
 ; PRIOR FILING DATE: 2000-05-01
 ; PRIOR APPLICATION NUMBER: 60/202,084
 ; PRIOR FILING DATE: 2000-05-04
 ; PRIOR APPLICATION NUMBER: 60/206,201
 ; PRIOR FILING DATE: 2000-05-22
 ; PRIOR APPLICATION NUMBER: 60/218,950
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: 60/222,903
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: 60/223,416
 ; PRIOR FILING DATE: 2000-08-04
 ; PRIOR APPLICATION NUMBER: 60/223,378
 ; PRIOR FILING DATE: 2000-08-07
 ; NUMBER OF SEQ ID NOS: 9597
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2271
 ; LENGTH: 100
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-796-692-2271

Query Match 100.0%; Score 81; DB 9; Length 100;
 Best Local Similarity 100.0%; Pred. No. 2.6e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTMPGFIADRMQK 15
 Db 46 GGTTMPGFIADRMQK 60

RESULT 3

US-10-040-862-1768
 ; Sequence 1768, Application US/10040862
 ; Publication No. US20030078396A1
 ; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Algate, Paul A.
 ; APPLICANT: Mannion, Jane
 ; APPLICANT: Retter, Marc
 ; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
 ; FILE REFERENCE: 014058-013520US
 ; CURRENT APPLICATION NUMBER: US/10/040,862
 ; CURRENT FILING DATE: 2001-11-06
 ; PRIOR APPLICATION NUMBER: US 60/186,126
 ; PRIOR FILING DATE: 2000-03-01
 ; PRIOR APPLICATION NUMBER: US 60/190,479
 ; PRIOR FILING DATE: 2000-03-17
 ; PRIOR APPLICATION NUMBER: US 60/200,545
 ; PRIOR FILING DATE: 2000-04-27
 ; PRIOR APPLICATION NUMBER: US 60/200,303
 ; PRIOR FILING DATE: 2000-04-28
 ; PRIOR APPLICATION NUMBER: US 60/200,779
 ; PRIOR FILING DATE: 2000-04-28
 ; PRIOR APPLICATION NUMBER: US 60/200,999
 ; PRIOR FILING DATE: 2000-05-01
 ; PRIOR APPLICATION NUMBER: US 60/202,084
 ; PRIOR FILING DATE: 2000-05-04
 ; PRIOR APPLICATION NUMBER: US 60/206,201
 ; PRIOR FILING DATE: 2000-05-22
 ; PRIOR APPLICATION NUMBER: US 60/218,950
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: US 60/222,903
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: US 60/223,416
 ; PRIOR FILING DATE: 2000-08-04
 ; PRIOR APPLICATION NUMBER: US 60/223,378
 ; PRIOR FILING DATE: 2000-08-07
 ; PRIOR APPLICATION NUMBER: US 09/796,692
 ; NUMBER OF SEQ ID NOS: 10467
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1768
 ; LENGTH: 100
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-040-862-1768

Query Match 100.0%; Score 81; DB 14; Length 100;
 Best Local Similarity 100.0%; Pred. No. 2.6e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTMPGFIADRMQK 15
 Db 46 GGTTMPGFIADRMQK 60

RESULT 4

US-10-040-862-2271
 ; Sequence 2271, Application US/10040862
 ; Publication No. US20030078396A1
 ; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Algate, Paul A.
 ; APPLICANT: Mannion, Jane
 ; APPLICANT: Retter, Marc
 ; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
 ; FILE REFERENCE: 014058-013520US
 ; CURRENT APPLICATION NUMBER: US/10/040,862
 ; CURRENT FILING DATE: 2001-11-06
 ; PRIOR APPLICATION NUMBER: US 60/186,126

```
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2271
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-2271
```

```
Query Match 100.0%; Score 81; DB 14; Length 100;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 GGTMYPGIADRMQK 15
Db 46 GGTMYPGIADRMQK 60
```

```
RESULT 5
US-10-057-475B-1768
; Sequence 1768, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2271
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-475B-2271
```

```
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1768
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-475B-1768
```

```
Query Match 100.0%; Score 81; DB 15; Length 100;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 GGTMYPGIADRMQK 15
Db 46 GGTMYPGIADRMQK 60
```

```
RESULT 6
US-10-057-475B-2271
; Sequence 2271, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2271
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-475B-2271
```

```

Query Match          100.0%; Score 81; DB 15; Length 100;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTMYPGIADRMOK 15
Db 46 GGTMYPGIADRMOK 60

RESULT 7
US-10-154-884B-1768
; Sequence 1768, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT FILING DATE: 2002-05-23
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1768
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-1768

Query Match          100.0%; Score 81; DB 15; Length 100;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTMYPGIADRMOK 15
Db 46 GGTMYPGIADRMOK 60

RESULT 8
US-10-154-884B-2271
; Sequence 2271, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT FILING DATE: 2002-05-23
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1768
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-1768

Query Match          100.0%; Score 81; DB 15; Length 100;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTMYPGIADRMOK 15
Db 46 GGTMYPGIADRMOK 60

RESULT 9
US-10-154-884B-2271
; Sequence 2271, Application US/10154884B
; Publication No. US20040175739A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT FILING DATE: 2004-01-23
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084

```

```

; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT FILING DATE: 2002-05-23
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2271
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-2271

Query Match          100.0%; Score 81; DB 15; Length 100;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTMYPGIADRMOK 15
Db 46 GGTMYPGIADRMOK 60

RESULT 9
US-10-154-884B-2271
; Sequence 1768, Application US/10764324
; Publication No. US20040175739A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT FILING DATE: 2004-01-23
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084

```

```
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1768
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-324-1768

Query Match      100.0%; Score 81; DB 16; Length 100;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTMYPGIADRMQK 15
   |||||
Db 46 GGTMYPGIADRMQK 60

RESULT 10
US-10-764-324-2271
; Sequence 2271, Application US/10764324
; Publication No. US20040175739A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-0135200S
; CURRENT APPLICATION NUMBER: US/10/764,324
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2271
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-324-2271

Query Match      100.0%; Score 81; DB 16; Length 100;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTMYPGIADRMQK 15
   |||||
Db 46 GGTMYPGIADRMQK 60

US-10-424-599-143033
; Sequence 143033, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 143033
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_100172C.1.pep
US-10-424-599-143033

Query Match      100.0%; Score 81; DB 15; Length 133;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTMYPGIADRMQK 15
   |||||
Db 59 GGTMYPGIADRMQK 73

RESULT 13
US-10-264-049-4259
; Sequence 4259, Application US/10264049
; Publication No. US2004000579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
```

```
Db 46 GGTMYPGIADRMQK 60

RESULT 11
US-10-264-049-4060
; Sequence 4060, Application US/10264049
; Publication No. US2004000579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4060
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-4060

Query Match      100.0%; Score 81; DB 15; Length 110;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTMYPGIADRMQK 15
   |||||
Db 36 GGTMYPGIADRMQK 50

RESULT 12
US-10-424-599-143033
; Sequence 143033, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 143033
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_100172C.1.pep
US-10-424-599-143033

Query Match      100.0%; Score 81; DB 15; Length 133;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTMYPGIADRMQK 15
   |||||
Db 59 GGTMYPGIADRMQK 73

RESULT 13
US-10-264-049-4259
; Sequence 4259, Application US/10264049
; Publication No. US2004000579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
```

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; FILE REFERENCE: PA133PI
; CURRENT APPLICATION NUMBER: US/10/264,049
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/19569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4259
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-4259

```

```

Query Match      100.0%; Score 81; DB 15; Length 145;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GGTMYPGIADRMOK 15
        |||||
Db      71 GGTMYPGIADRMOK 85

```

```

RESULT 14
US-09-796-692-1239
; Sequence 1239, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1239
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-692-1239

```

```

Query Match      100.0%; Score 81; DB 9; Length 147;
Best Local Similarity 100.0%; Pred. No. 4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GGTMYPGIADRMOK 15
        |||||
Db      73 GGTMYPGIADRMOK 87

```

```

RESULT 15
US-09-796-692-1696
; Sequence 1696, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1696
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-692-1696

```

```

Query Match      100.0%; Score 81; DB 9; Length 147;
Best Local Similarity 100.0%; Pred. No. 4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GGTMYPGIADRMOK 15
        |||||
Db      73 GGTMYPGIADRMOK 87

```

```

Search completed: April 8, 2005, 12:50:58
Job time : 43.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 9.33333 Seconds
(without alignments)
154.634 Million cell updates/sec

Title: US-09-423-351C-4
Perfect score: 81
Sequence: 1 GGTTMPGIADRMQK 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	100.0	71	139393	alpha-actin - huma
2	81	100.0	100	14851	actin - fruit fly
3	81	100.0	125	A26337	actin, skeletal mu
4	81	100.0	195	S39777	actin beta - pig (
5	81	100.0	213	A61043	actin CA15 - sea s
6	81	100.0	308	A03000	actin 3 - fruit fl
7	81	100.0	328	S05430	actin beta - grass
8	81	100.0	349	B25819	actin, fetal skele
9	81	100.0	362	A26559	actin type 5, cyto
10	81	100.0	374	1 ATRBOB	actin beta - bovin
11	81	100.0	374	1 ATRBOG	actin gamma - bovi
12	81	100.0	374	2 JC5818	gamma-actin - huma
13	81	100.0	375	1 ATRQSM	actin, aortic smoo
14	81	100.0	375	1 ATRB	actin, skeletal mu
15	81	100.0	375	1 ATRTC	actin beta - rat
16	81	100.0	375	1 A48324	actin beta, cytosk
17	81	100.0	375	1 ATRCHB	actin beta - chick
18	81	100.0	375	1 ATRHUB	actin beta - human
19	81	100.0	375	1 ATRHUG	actin gamma 1 - hu
20	81	100.0	375	1 ATRMSB	actin beta - mouse
21	81	100.0	375	1 ATRMSG	actin gamma - mous
22	81	100.0	375	1 ATRBB	actin beta, non-mu
23	81	100.0	375	1 S11222	actin gamma, cytos
24	81	100.0	375	2 S33386	actin, cytosolic (
25	81	100.0	375	2 S47897	actin 1 - Pneumocy
26	81	100.0	375	2 A26836	actin - fission ye
27	81	100.0	375	2 S71125	actin beta-2, cyto
28	81	100.0	375	2 S71124	actin beta-1, cyto
29	81	100.0	375	2 S71126	actin beta, cyto

actin beta - goose
actin alpha, Cardi
actin - imperfect
actin 7 - fruit fl
actin gamma, cytos
actin gamma, smoot
Actin-1A - nematod
actin 8 - fruit fl
actin 87E - fruit
actin - fruit fly
actin gamma, enter
actin - pork tapew
actin 4 - Caenorha
actin 1 and actin
actin 2 - Caenorha
hypothetical prote

ALIGNMENTS

RESULT 1

139393
alpha-actin - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C:Accession: I39393
R:Fuchs, E.; Kim, K.H.; Hanukoglu, I.; Tanese, N.
Curr. Probl. Dermatol. 11, 27-44, 1983
A:Title: The evolution and complexity of the genes encoding the cytoskeletal proteins of
A:Reference number: I39393; MUID:84083477; PMID:6686106
A:Accession: I39393
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-71 <RES>
A:Cross-references: UNIPROT:Q9UE89; GB:M28424; NID:gl78023; PIDN:AAB16906.1; PID:gl78024
C:Superfamily: actin

Query Match 100.0%; Score 81; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 7.8e-07; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;

Qy 1 GGTTMPGIADRMQK 15
Db 40 GGTTMPGIADRMQK 54

RESULT 2

14851
actin - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S14851
R:Burn, T.C.; Tobin, S.L.
submitted to the EMBL Data Library, October 1990
A:Reference number: S14851
A:Accession: S14851
A:Molecule type: DNA
A:Residues: 1-100 <BUR>
A:Cross-references: UNIPROT:P02572; EMBL:X54848; NID:g7549; PIDN:CAA38618.1; PID:g7550
C:Genetics:

A:Gene: FlyBase:Act42A
A:Cross-references: FlyBase:FBgn0000043
C:Superfamily: actin

C:Keywords: cell motility; cytoskeleton; microfilament; mitosis; structural protein

Query Match 100.0%; Score 81; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.1e-06; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;

Qy 1 GGTTMPGIADRMQK 15
Db 26 GGTTMPGIADRMQK 40

RESULT 3

A26337
 actin, skeletal muscle - Iberian ribbed newt (fragment)
 C:Species: Pleurodeles waltl (Iberian ribbed newt)
 C>Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
 C:Accession: A26337
 R:Khrstchatskiy, M.; Pontes, M.
 J. Mol. Biol. 193, 409-412, 1987
 A:Title: There is an alpha-actin skeletal muscle-specific gene in a salamander (Pleurodeles waltl)
 A:Reference number: A26337; MUID:87254218; PMID:3453122
 A:Accession: A26337
 A:Molecule type: DNA
 A:Residues: 1-125 <KRP>
 A:CROSS-references: UNIPROT:P10994; GB:X05106; NID:964248; PID:CAA28753.1; PID:964249
 C:Superfamily: actin
 C:Keywords: muscle; skeletal muscle

Query Match 100.0%; Score 81; DB 2; Length 125;
 Best Local Similarity 100.0%; Pred. No. 1.4e-06; Mismatches 0; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTMYPGIADRMQK 15
 |||||
 DB 51 GGTMYPGIADRMQK 65

RESULT 4

S39777
 actin beta - pig (fragments)
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
 C:Accession: S39777
 R:Adamski, J.; Hussen, B.; Thole, H.H.; Groeschel-Stewart, U.; Jungblut, P.W.
 Biochem. J. 296, 797-802, 1993
 A:Title: Linkage of 17-beta-estradiol dehydrogenase to actin by epsilon-(gamma-glutamyl-1-ATP)
 A:Reference number: S39777; MUID:94107247; PMID:8280079
 A:Accession: S39777
 A:Molecule type: protein
 A:Residues: 1-20;21-52;53-79;80-85;86-95;96-116;117-151;152-159;160-195 <ADA>
 A:CROSS-references: UNIPROT:Q7M3B0
 C:Superfamily: actin

Query Match 100.0%; Score 81; DB 2; Length 195;
 Best Local Similarity 100.0%; Pred. No. 2.2e-06; Mismatches 0; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTMYPGIADRMQK 15
 |||||
 DB 126 GGTMYPGIADRMQK 140

RESULT 5

A61043
 actin CA15 - sea squirt (Styela clava) (fragments)
 C:Species: Styela clava
 C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C:Accession: A61043
 R:Seach, R.L.; Jeffery, W.R.
 Dev. Genet. 11, 2-14, 1990
 A:Title: Temporal and spatial expression of a cytoskeletal actin gene in the ascidian Styela clava
 A:Reference number: A61043; MUID:90298580; PMID:2361333
 A:Accession: A61043
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-213 <BEA>
 A:CROSS-references: UNIPROT:Q7M3Y7
 C:Comment: This sequence is expressed in cells undergoing rapid cell division.
 C:Superfamily: actin
 C:Keywords: cytoskeleton; methylated amino acid; mitosis; structural protein
 F;73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 81; DB 2; Length 213;
 Best Local Similarity 100.0%; Pred. No. 2.4e-06; Mismatches 0; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTMYPGIADRMQK 15
 |||||
 DB 139 GGTMYPGIADRMQK 153

RESULT 6

A03000
 actin 3 - fruit fly (Drosophila melanogaster) (fragments)
 C:Species: Drosophila melanogaster
 C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
 C:Accession: A03000
 R:Fyberg, E.A.; Bond, B.J.; Hershey, N.D.; Mixter, K.S.; Davidson, N.
 Cell 24, 107-116, 1981
 A:Title: The actin genes of Drosophila: protein coding regions are highly conserved but
 A:Reference number: A03000; MUID:81210174; PMID:6263481
 A:Accession: A03000
 A:Molecule type: DNA
 A:Residues: 1-308 <FYR>
 A:CROSS-references: UNIPROT:P02572
 A:Note: there are 68 unsequenced residues between positions 160 and 161. Partial sequence
 A:Note: the authors translated the codon GTT for residue 263 as Ile
 C:Genetics:

A:Gene: FlyBase:Act42A
 A:CROSS-references: FlyBase:FBgn0000043
 A:Map position: 42A
 C:Superfamily: actin
 C:Keywords: methylated amino acid
 F;74/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 81; DB 2; Length 308;
 Best Local Similarity 100.0%; Pred. No. 3.6e-06; Mismatches 0; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTMYPGIADRMQK 15
 |||||
 DB 234 GGTMYPGIADRMQK 248

RESULT 7

S05430
 actin beta - grass carp
 C:Species: Ctenopharyngodon idella (grass carp)
 C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
 C:Accession: S05430
 R:Liu, Z.; Zhu, Z.; Roberg, K.; Faras, A.J.; Guise, K.S.; Kapuscinski, A.R.; Hackett, P.
 Nucleic Acids Res. 17, 5850, 1989
 A:Title: The beta-actin gene of carp (Ctenopharyngodon idella).
 A:Reference number: S05430; MUID:89345185; PMID:2762162
 A:Accession: S05430
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-328 <LIU>
 A:CROSS-references: UNIPROT:P83751; EMBL:M25013
 C:Genetics:
 A:introns: 41/3; 121/3; 268/1

C:Keywords: cytoskeleton; methylated amino acid
 F;73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 81; DB 2; Length 328;
 Best Local Similarity 100.0%; Pred. No. 3.8e-06; Mismatches 0; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTMYPGIADRMQK 15
 |||||
 DB 301 GGTMYPGIADRMQK 315

RESULT 8

B25819
 actin, fetal skeletal/adult cardiac muscle - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 09-Jul-2004
 C:Accession: B25819
 R:Alonso, S.; Minty, A.; Bourlet, Y.; Buckingham, M.
 J. Mol. Evol. 23, 11-22, 1986
 A>Title: Comparison of three actin-coding sequences in the mouse; evolutionary relations
 A:Reference number: A25819; MUID:86200234; PMID:3084797
 A:Accession: B25819
 A:Molecule type: mRNA
 A:Residues: 1-349 <ALO>
 A:Cross-references: UNIPROT:Q61275; GB:J030381; GB:M10652; NID:G49869; PIDN:CA
 C:Superfamily: actin
 C:Keywords: cardiac muscle; heart; methylated amino acid; muscle; skeletal muscle
 F:47/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 81; DB 2; Length 349;
 Best Local Similarity 100.0%; Pred. No. 4.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTMYPGIADRMQK 15
 |||||
 Db 275 GGTMYPGIADRMQK 289

RESULT 9
 A26559
 actin type 5, cytosolic - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 09-Sep-1987 #sequence_revision 09-Sep-1987 #text_change 05-Dec-1997
 C:Accession: A26559
 R:Bergsma, D.J.; Chang, K.S.; Schwartz, R.J.
 Mol. Cell. Biol. 5, 1151-1162, 1985
 A:Reference number: A26559; MUID:85213487; PMID:4000121
 A:Accession: A26559
 A:Molecule type: DNA
 A:Residues: 1-362 <BER>
 C:Superfamily: actin
 C:Keywords: cytosol; methylated amino acid
 F:74/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 81; DB 2; Length 362;
 Best Local Similarity 100.0%; Pred. No. 4.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTMYPGIADRMQK 15
 |||||
 Db 302 GGTMYPGIADRMQK 316

RESULT 10
 A7BOB
 actin beta - bovine (tentative sequence)
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
 C:Accession: E14185; A39105; A02999; A14185
 R:Vandekerckhove, J.; Weber, K.
 Eur. J. Biochem. 90, 451-462, 1978
 A>Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain
 A:Reference number: A14185; MUID:79045349; PMID:213279
 A:Accession: E14185
 A:Molecule type: protein
 A:Residues: 1-374 <VAN>
 A:Cross-references: UNIPROT:P60712
 A>Note: only peptides that differed in composition from the corresponding peptides of ra
 R:Degen, J.L.; Neubauer, M.G.; Degen, S.J.F.; Seyfried, C.B.; Morris, D.R.
 J. Biol. Chem. 258, 12153-12162, 1983
 A>Title: Regulation of protein synthesis in mitogen-activated bovine lymphocytes. Analys
 A:Reference number: A39105; MUID:84032385; PMID:6195151
 A:Accession: A39105
 A:Molecule type: mRNA
 A:Residues: 76-227;344-374 <DEG>

A:Cross-references: GB:K00622; GB:K00623
 A>Note: actins beta and gamma were not distinguished in this study
 C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
 C:Superfamily: actin
 C:Keywords: blocked amino end; cell motility; cytoskeleton; methylated amino acid; micro
 F:1/Modified site: blocked amino end (Asp) (probably acetylated) #status experimental
 F:72/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 81; DB 1; Length 374;
 Best Local Similarity 100.0%; Pred. No. 4.4e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTMYPGIADRMQK 15
 |||||
 Db 300 GGTMYPGIADRMQK 314

RESULT 11
 A7BOG
 actin gamma - bovine (tentative sequence)
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
 C:Accession: E14185; A02999
 R:Vandekerckhove, J.; Weber, K.
 Eur. J. Biochem. 90, 451-462, 1978
 A>Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain
 A:Reference number: A14185; MUID:79045349; PMID:213279
 A:Accession: E14185
 A:Molecule type: protein
 A:Residues: 1-374 <VAN>
 A:Cross-references: UNIPROT:P02571
 A>Note: only peptides that differed in composition from the corresponding peptides of ra
 C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
 C:Superfamily: actin
 C:Keywords: blocked amino end; cell motility; cytoskeleton; methylated amino acid; micro
 F:1/Modified site: blocked amino end (Glu) (probably acetylated) #status experimental
 F:72/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 81; DB 1; Length 374;
 Best Local Similarity 100.0%; Pred. No. 4.4e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTMYPGIADRMQK 15
 |||||
 Db 300 GGTMYPGIADRMQK 314

RESULT 12
 JC5818
 gamma-actin - human
 C:Species: Homo sapiens (man)
 C>Date: 20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
 C:Accession: JC5818; PC4501
 R:Hauschildt, S.; Schwarz, C.; Heine, H.; Ulmer, A.J.; Flad, H.D.; Rietschel, E.T.; Jens
 Biochem. Biophys. Res. Commun. 241, 670-674, 1997
 A>Title: Actin: A target of lipopolysaccharide-induced phosphorylation in human monocytes
 A:Reference number: JC5818; MUID:98096379; PMID:9434766
 A:Accession: JC5818
 A:Molecule type: protein
 A:Residues: 1-374 <HAU>
 A:Cross-references: UNIPROT:P02571
 A:Experimental source: monocyte
 A:Accession: PC4501
 A:Molecule type: protein
 A:Residues: 1-61;84-112;147-190;196-209;215-253;335-358 <HA2>
 A:Experimental source: monocyte
 C:Comment: This protein is involved in a signal transduction that eventually leads to mo
 C:Superfamily: actin

Query Match 100.0%; Score 81; DB 2; Length 374;
 Best Local Similarity 100.0%; Pred. No. 4.4e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTMYPGIADRMQK 15
 |||||
 Db 300 GGTTMYPGIADRMQK 314

RESULT 13
 A:Title: aortic smooth muscle - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 06-Sep-1996
 C:Accession: A02997; S13480
 R:Vandekerckhove, J.; Weber, K.
 Differentiation 14, 123-133, 1979
 A:Title: The complete amino acid sequence of actins from bovine aorta, bovine heart, bovine thymus.
 A:Reference number: A02997; PMID:80047657; PMID:499690
 A:Accession: A02997
 A:Molecule type: protein
 A:Residues: 1-375 <VAN>
 R:Zevgolis, V.G.; Sotiropoulos, T.G.; Evangelopoulos, A.E.
 Biochim. Biophys. Acta 1091, 222-230, 1991
 A:Title: Phosphorylase kinase from bovine stomach smooth muscle: a Ca (2+)-dependent protein
 A:Reference number: S13480; PMID:91137633; PMID:1995080
 A:Accession: S13480
 A:Molecule type: protein
 A:Residues: 40-49 <ZEV>
 A:Experimental source: stomach
 A:Note: This material appears to be actin of aortic smooth muscle type or a related molecule
 C:Superfamily: actin
 C:Keywords: acetylated amino end; methylated amino acid; muscle contraction
 F:1/Modified site: acetylated amino end (Glu) #status predicted
 F:73/Modified site: 3'-methylhistidine (His) #status experimental

Query Match 100.0%; Score 81; DB 1; Length 375;
 Best Local Similarity 100.0%; Pred. No. 4.4e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTMYPGIADRMQK 15
 |||||
 Db 301 GGTTMYPGIADRMQK 315

RESULT 14
 A:Title: skeletal muscle - rabbit
 N:Alternate names: F-actin
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 07-May-1999
 C:Accession: A92182; A14185; S65873; S70610; S44393; A02994
 R:Collins, J.H.; Elzinga, M.
 J. Biol. Chem. 250, 5915-5920, 1975
 A:Title: The primary structure of actin from rabbit skeletal muscle. Completion and analysis of the primary structure of actin from rabbit skeletal muscle. Completion and analysis of the primary structure of actin from rabbit skeletal muscle.
 A:Reference number: A92182; PMID:75211334; PMID:1150665
 A:Accession: A92182
 A:Molecule type: protein
 A:Residues: 1-2, 'T', 'D', '6-11', 'D', '13-73', 'W', '74-78, 80-234, 236-308, 'T', 310-375 <COL>
 A:Note: this is the final paper in a series
 A:Note: this sequence has been revised in references A14185 and A90406
 R:Vandekerckhove, J.; Weber, K.
 Eur. J. Biochem. 90, 451-462, 1978
 A:Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain and rabbit skeletal muscle.
 A:Reference number: A14185; PMID:79045349; PMID:213279
 A:Accession: A14185
 A:Molecule type: protein
 A:Residues: 1-18; 69-84 <VAN>
 R:Lu, R.C.; Elzinga, M.
 Biochemistry 16, 5801-5806, 1977
 A:Title: Partial amino acid sequence of brain actin and its homology with muscle actin.
 A:Reference number: A90406; PMID:78060866; PMID:588555
 A:Contents: annotation
 A:Note: residue 235 has been added and residue 309 has been revised
 R:Vandat, A.; Miller, C.; Phillips, M.; Muhlrad, A.; Reisler, E.
 FEBS Lett. 365, 149-151, 1995

A:Title: A novel 27/16 kDa form of subtilisin cleaved actin: structural and functional characterization
 A:Reference number: S65873; PMID:95300963; PMID:7781768
 A:Accession: S65873
 A:Molecule type: protein
 A:Residues: 235-241 <VAH>
 R:Strzelecka-Golaszewska, H.; Wozniak, A.; Hult, T.; Lindberg, U.
 Biochem. J. 316, 713-721, 1996
 A:Title: Effects of the type of divalent cation, Ca2+ or Mg2+, bound at the high-affinity binding site on the actin-myosin complex
 A:Reference number: S70610; PMID:96265033; PMID:8670143
 A:Accession: S70610
 A:Molecule type: protein
 A:Residues: 48-54; 68-72; 235-243 <STR>
 A:Experimental source: skeletal muscle
 R:Bertrand, R.; Derancourt, J.; Kassab, R.
 FEBS Lett. 345, 113-119, 1994
 A:Title: The covalent maleimidebenzoyl-actin-myosin head complex. Cross-linking of the 50 kDa actin-myosin complex
 A:Reference number: S44393; PMID:94259162; PMID:8200441
 A:Accession: S44393
 A:Molecule type: protein
 A:Residues: 48-64 <BER>
 A:Experimental source: skeletal muscle
 C:Superfamily: actin
 C:Keywords: acetylated amino end; ATP binding; methylated amino acid; muscle contraction
 F:1-375/Product: actin #status experimental <MAT>
 F:1/Modified site: acetylated amino end (Asp) #status experimental
 F:73/Modified site: 3'-methylhistidine (His) #status experimental

Query Match 100.0%; Score 81; DB 1; Length 375;
 Best Local Similarity 100.0%; Pred. No. 4.4e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTMYPGIADRMQK 15
 |||||
 Db 301 GGTTMYPGIADRMQK 315

RESULT 15
 A:Title: actin beta - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 22-Jun-1999
 C:Accession: A38571; A02999
 R:Nudel, U.; Zakut, R.; Shani, M.; Neuman, S.; Levy, Z.; Yaffe, D.
 Nucleic Acids Res. 11, 1759-1771, 1983
 A:Title: The nucleotide sequence of the rat cytoplasmic beta-actin gene.
 A:Reference number: A38571; PMID:83168920; PMID:6300777
 A:Accession: A38571
 A:Molecule type: DNA
 A:Residues: 1-375 <NUD>
 A:Cross-references: GB:J00691; NID:G202653; PIDN:AAA40657.1; PID:G202654
 C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins, actin beta and actin gamma.
 C:Genetics: 41/3; 121/3; 268/1; 328/3
 C:Introns: 41/3; 121/3; 268/1; 328/3
 C:Superfamily: actin
 C:Keywords: cell motility; cytoskeleton; methylated amino acid; microfilament; mitosis; F-actin
 F:2-375/Product: actin beta #status predicted <MAT>
 F:73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 81; DB 1; Length 375;
 Best Local Similarity 100.0%; Pred. No. 4.4e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTMYPGIADRMQK 15
 |||||
 Db 301 GGTTMYPGIADRMQK 315

Search completed: April 8, 2005, 10:53:05
 Job time : 9.33333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 57.8667 Seconds
(without alignments)
132.739 Million cell updates/sec

Title: US-09-423-351C-4
Perfect score: 81
Sequence: 1 GGTTMYPGIADRMQK 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	60	Q95164	Q95164 canis famil
2	81	100.0	71	Q9UE89	Q9UE89 homo sapien
3	81	100.0	93	Q7ZZ20	Q7ZZ20 anas platyr
4	81	100.0	96	Q90X51	Q90X51 fundulus he
5	81	100.0	100	Q9TYD9	Q9TYD9 styela clav
6	81	100.0	103	Q95YGS	Q95YGS apis cerana
7	81	100.0	106	Q80UA7	Q80UA7 marmota mon
8	81	100.0	107	Q8J1Q2	Q8J1Q2 anguilla ja
9	81	100.0	109	Q91877	Q91877 diprion pin
10	81	100.0	109	Q91881	Q91881 diadromus p
11	81	100.0	110	Q76493	Q76493 bemisia arg
12	81	100.0	111	Q6R127	Q6R127 boophilus m
13	81	100.0	111	Q6R128	Q6R128 boophilus m
14	81	100.0	113	Q6Y260	Q6Y260 pagrus majo
15	81	100.0	118	Q9DF22	Q9DF22 scyllorhinu
16	81	100.0	123	Q6UIS1	Q6UIS1 macaca mula
17	81	100.0	123	Q6UIS2	Q6UIS2 pan troglod
18	81	100.0	124	Q6B9W6	Q6B9W6 parastromy
19	81	100.0	124	Q95319	Q95319 sus scrofa
20	81	100.0	124	Q9DFK3	Q9DFK3 gillichthys
21	81	100.0	125	1 ACTS PLEWA	10994 pleurodeles
22	81	100.0	129	Q9NAY5	Q9NAY5 papilio can
23	81	100.0	131	Q9XSB1	Q9XSB1 tupia glis
24	81	100.0	133	Q96104	Q96104 apis mellif
25	81	100.0	134	Q99NC5	Q99NC5 mus musculu
26	81	100.0	134	Q99NC6	Q99NC6 rattus norv
27	81	100.0	141	Q9NAY6	Q9NAY6 papilio gla
28	81	100.0	141	Q6PT58	Q6PT58 squalus aca
29	81	100.0	141	Q6Q6W9	Q6Q6W9 ictalurus p
30	81	100.0	145	Q6B9V8	Q6B9V8 strongyloid
31	81	100.0	149	Q6PTC1	Q6PTC1 sitobion av

32	81	100.0	149	2	Q6PTC2	Q6PTC2 sitobion av
33	81	100.0	159	2	Q96DE1	Q96DE1 homo sapien
34	81	100.0	159	2	Q9DG95	Q9DG95 pagrus majo
35	81	100.0	165	2	Q96FUG	Q96FUG homo sapien
36	81	100.0	170	2	Q966R4	Q966R4 chironomus
37	81	100.0	171	2	Q6GXB6	Q6GXB6 lepisosteus
38	81	100.0	171	2	Q7ZW59	Q7ZW59 rana cateeb
39	81	100.0	176	2	Q96CV5	Q96CV5 drosophila
40	81	100.0	176	2	Q96FV8	Q96FV8 drosophila
41	81	100.0	181	2	Q6XJ33	Q6XJ33 drosophila
42	81	100.0	183	2	Q9YGY6	Q9YGY6 orochromis
43	81	100.0	195	2	Q7M3B0	Q7M3B0 sus scrofa
44	81	100.0	207	2	Q6SQL9	Q6SQL9 helicon pel
45	81	100.0	213	2	Q7M3Y7	Q7M3Y7 styela clav

ALIGNMENTS

RESULT 1
Q95164 PRELIMINARY; PRT; 60 AA.
AC Q95164;
DT 01-FEB-1997 (Tremblrel. 02, Created)
DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Beta-actin (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97008128; PubMed=8855304; DOI=10.1073/pnas.93.20.11035;
RA Lee Y.A., Liang C.S., Lee M.A., Lindpaintner K.;
RT "Local stress, not systemic factors, regulate gene expression of the
cardiac renin-angiotensin system in vivo: a comprehensive study of all
its components in the dog."
RL Proc. Natl. Acad. Sci. U.S.A. 93:11035-11040(1996).
DR EMBL; U67202; AAC48640.1; -
DR HSSP; P02568; IMA9.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
FT pfam: PF00022; Actin; 1.
FT NON_TER 1
FT NON_TER 60
SQ SEQUENCE 60 AA; 6744 MW; AA02DE065D32D7C4 CRC64;

Query Match 100.0%; Score 81; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGTTMYPGIADRMQK 15
|||
Db 20 GGTTMYPGIADRMQK 34
|||

RESULT 2
Q9UE89 PRELIMINARY; PRT; 71 AA.
AC Q9UE89;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Beta-actin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Foreskin;

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RX MEDLINE=84083477; PubMed=6686106;
RA Fuchs E., Kim K.H., Hanukoglu I., Tanase N.;
RT "The evolution and complexity of the genes encoding the cytoskeletal
RT proteins of human epidermal cells.";
RL Curr. Probl. Dermatol. 11:27-44(1983).
DR EMBL; M28424; AAB16906.1; -.
DR PIR; I39393; I39393.
DR HSP; P02568; 1MA9.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON TER 1
FT NON TER 71
SQ SEQUENCE 71 AA; 7799 MW; D3886403C855CF70 CRC64;

Query Match 100.0%; Score 81; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 5.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTMYPGIADRMQK 15
Db 40 GGTMYPGIADRMQK 54

RESULT 3
Q7ZZZ0
ID Q7ZZZ0 PRELIMINARY; PRT; 93 AA.
AC Q7ZZZ0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-actin (Fragment).
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Sreekumar E., Premraj A., Rasool T.J.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY251275; AAP04479.1; -.
DR HSP; P02568; 1QZ5.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PROSITE; PS00432; ACTINS_2; 1.
FT NON TER 1
FT NON TER 93
SQ SEQUENCE 93 AA; 10444 MW; F867ADF144D80523 CRC64;

Query Match 100.0%; Score 81; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 7.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTMYPGIADRMQK 15
Db 19 GGTMYPGIADRMQK 33

RESULT 4
Q90X51
ID Q90X51 PRELIMINARY; PRT; 96 AA.
AC Q90X51;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta-actin (Fragment).
OS Fundulus heteroclitus (Killifish) (Mummichog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Fundulidae; Fundulus.
RN NCBI_TaxID=8078;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Roling J.A., Baldwin W.S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF355092; AAL29465.1; -.
DR HSP; P02568; 1QZ5.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR Pfam; PF00022; Actin; 1.
DR PROSITE; PS00432; ACTINS_2; 1.
FT NON TER 1
FT NON TER 96
SQ SEQUENCE 96 AA; 10798 MW; 7440DA6AE5A070C4 CRC64;

Query Match 100.0%; Score 81; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 8.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTMYPGIADRMQK 15
Db 33 GGTMYPGIADRMQK 47

RESULT 5
Q9TVD9
ID Q9TVD9 PRELIMINARY; PRT; 100 AA.
AC Q9TVD9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-muscle actin (Fragment).
GN Name=Tb24;
OS Styela clava (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Styelidae; Styela.
OX NCBI_TaxID=7725;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92249656; PubMed=1577198;
RA Beach R.L., Jeffery W.R.;
RT "Multiple actin genes encoding the same alpha-muscle isoform are
RT expressed during ascidian development.";
RL Dev. Biol. 151:55-66(1992).
DR EMBL; L13788; AAA29846.1; -.
DR HSP; P02568; 1QZ5.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PROSITE; PS00432; ACTINS_2; 1.
FT NON TER 1
FT NON TER 100
SQ SEQUENCE 100 AA; 11264 MW; 108CE34548BABB5E CRC64;

Query Match 100.0%; Score 81; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 8.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTMYPGIADRMQK 15
Db 26 GGTMYPGIADRMQK 40

RESULT 6
Q95YG5
ID Q95YG5 PRELIMINARY; PRT; 103 AA.
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Q95YG5;
AC 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Actin (Fragment).
OS Apis cerana (Indian honeybee).
OC Neoptera; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7461;
RN [1]
RP SEQUENCE FROM N.A.
RA Shimizu I., Kawai Y., Taniguchi M., Aoki S.;
RT "Circadian rhythm and cDNA cloning of the clock gene period in the
RT honeybee Apis cerana japonica.";
RL Zool. Sci. 18:779-789(2001).
DR EMBL; AB072495; BAB69483.1; -.
DR HSSP; P10983; 1D4X.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 1
FT NON_TER 103
SQ SEQUENCE 103 AA; 11520 MW; 5203DA3630FCD807 CRC64;

Query Match 100.0%; Score 81; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 8.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTMPGIADRMQK 15
Db 66 GGTTMPGIADRMQK 80
|||||
RESULT 7
Q80UA7
ID Q80UA7 PRELIMINARY; PRT; 106 AA.
AC Q80UA7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-actin (Fragment).
OS Maxmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22554704; PubMed=12668969; DOI=10.1053/jhep.2003.50154;
RA Wang Y., Menne S., Jacob J.R., Tennant B.C., Gerin J.L., Cote P.J.;
RT "Role of type 1 versus type 2 immune responses in liver during the
RT onset of chronic woodchuck hepatitis virus infection.";
RL Hepatology 37:771-780(2003).
DR EMBL; AV170121; AAO39434.1; -.
DR HSSP; P10983; 1D4X.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PROSITE; PS00432; ACTINS_2; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 106 AA; 11864 MW; 9PFD3C145651FE343 CRC64;

Query Match 100.0%; Score 81; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 8.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTMPGIADRMQK 15
Db 66 GGTTMPGIADRMQK 80
|||||
RESULT 7
Q80UA7
ID Q80UA7 PRELIMINARY; PRT; 106 AA.
AC Q80UA7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-actin (Fragment).
OS Maxmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22554704; PubMed=12668969; DOI=10.1053/jhep.2003.50154;
RA Wang Y., Menne S., Jacob J.R., Tennant B.C., Gerin J.L., Cote P.J.;
RT "Role of type 1 versus type 2 immune responses in liver during the
RT onset of chronic woodchuck hepatitis virus infection.";
RL Hepatology 37:771-780(2003).
DR EMBL; AV170121; AAO39434.1; -.
DR HSSP; P10983; 1D4X.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PROSITE; PS00432; ACTINS_2; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 106 AA; 11864 MW; 9PFD3C145651FE343 CRC64;

Query Match 100.0%; Score 81; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 8.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTMPGIADRMQK 15
Db 66 GGTTMPGIADRMQK 80
|||||

Db 32 GGTTMPGIADRMQK 46
RESULT 8
Q8JQ2
ID Q8JQ2 PRELIMINARY; PRT; 107 AA.
AC Q8JQ2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta-actin (Fragment).
GN Name=b-act;
OS Anguilla japonica (Japanese eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC Anguilla.
OX NCBI_TaxID=7937;
RN [1]
RP SEQUENCE FROM N.A.
RA Kurokawa T.;
RT Tissue=Pancreas;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB074846; BAB96533.1; -.
DR HSSP; P10983; 1D4X.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 12006 MW; 375A7A5C6E6CEA3A CRC64;

Query Match 100.0%; Score 81; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTMPGIADRMQK 15
Db 67 GGTTMPGIADRMQK 81
|||||
RESULT 9
P91877
ID P91877 PRELIMINARY; PRT; 109 AA.
AC P91877;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Actin (Fragment).
OS Diprion pini.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Tenthredinoidea; Diprionidae;
OC Diprion.
OX NCBI_TaxID=52634;
RN [1]
RP SEQUENCE FROM N.A.
RA Hamelin E., Bigot Y.Y.B., Rouleux F., Renault S., Periquet G.;
RT Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
[2]
RA Bigot Y.B.;
RP Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
RL EMBL; X91507; CAA62807.1; -.
DR HSSP; P10983; 1D4X.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 12036 MW; 15F3926B8D263554 CRC64;

Query Match 100.0%; Score 81; DB 2; Length 109;

Best Local Similarity 100.0%; Pred. No. 9.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTMYPGIADRMQK 15
|||||
Db 54 GGTMYPGIADRMQK 68

RESULT 10

ID P91881 PRELIMINARY; PRT; 109 AA.
AC P91881;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Actin (Fragment).
OS Diadromus pulchellus (Parasitic wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;
OC Ichneumonidae; Ichneumoninae; Diadromus.
OX NCBI_TaxID=7420;
RN [1]
RP SEQUENCE FROM N.A.
RA Hamelin E., Bigot Y.Y.B., Rouleux F., Renault S., Periquet G.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Bigot Y.B.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; X91506; CAA62806.1; -.
DR HSSP; P10983; 1D4X.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 12251 MW; 3C34D292C5AA039A CRC64;

Query Match 100.0%; Score 81; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 9.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTMYPGIADRMQK 15
|||||
Db 54 GGTMYPGIADRMQK 68

RESULT 11

ID O76493 PRELIMINARY; PRT; 110 AA.
AC O76493;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Actin (Fragment).
OS Bemisia argentifolii (silverleaf whitefly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aleyrodiformes;
OC Aleyrodidae; Aleyrodinae; Bemisia.
OX NCBI_TaxID=77855;
RN [1]
RP SEQUENCE FROM N.A.
RA He M., Haymer D.S., Lai P.Y.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF071908; AAC24152.1; -.
DR HSSP; P10983; 1D4X.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 1
FT NON_TER 110

SQ SEQUENCE 110 AA; 12070 MW; DD2831BC3D4D3EF8 CRC64;

Query Match 100.0%; Score 81; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 9.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTMYPGIADRMQK 15
|||||
Db 75 GGTMYPGIADRMQK 89

RESULT 12

ID Q6R127 PRELIMINARY; PRT; 111 AA.
AC Q6R127;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Beta-actin (Fragment).
OS Boophilus microplus (Cattle tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Boophilus.
OX NCBI_TaxID=6941;
RN [1]
RP SEQUENCE FROM N.A.
RA Holmes S.P., Barron P.D., He H., Pietrantonio P.V.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY519367; AAS09968.1; -.
FT NON_TER 1
FT NON_TER 111
SQ SEQUENCE 111 AA; 12310 MW; 5639572768E148F5 CRC64;

Query Match 100.0%; Score 81; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 9.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTMYPGIADRMQK 15
|||||
Db 69 GGTMYPGIADRMQK 83

RESULT 13

ID Q6R128 PRELIMINARY; PRT; 111 AA.
AC Q6R128;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Beta-actin (Fragment).
OS Boophilus microplus (Cattle tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Boophilus.
OX NCBI_TaxID=6941;
RN [1]
RP SEQUENCE FROM N.A.
RA Holmes S.P., Barron P.D., He H., Pietrantonio P.V.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY519366; AAS09967.1; -.
FT NON_TER 1
FT NON_TER 111
SQ SEQUENCE 111 AA; 12294 MW; 40F58D31A43B48F5 CRC64;

Query Match 100.0%; Score 81; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 9.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTMYPGIADRMQK 15
|||||
Db 69 GGTMYPGIADRMQK 83

RESULT 14

O6Y260

Search completed: April 8, 2005, 12:03:08
Job time : 59.8667 secs

```
ID Q6Y260 PRELIMINARY; PRT; 113 AA.
AC Q6Y260;
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE Alpha-actin protein (Fragment).
OS Pagrus major (Red sea bream) (Chrysophrys major).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Pagrus.
OX NCBI_TaxID=143350;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Chen S.L., Xu M.Y., Hu S.L., Li L.;
RT "Analysis of immune-relevant genes expressed in red sea bream
RL Aquaculture 240:115-130(2004).
RL EMBL; AY190676; AAP20152.1; -.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR PROSITE; PS00432; ACTINS_2; 1.
FT NON_TER 1
SQ SEQUENCE 113 AA; 12550 MW; 4C796A5B5B35269F CRC64;

Query Match 100.0%; Score 81; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 9.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTMYPGIADRMQK 15
Db 39 GGTMYPGIADRMQK 53

RESULT 15
Q9DF22 PRELIMINARY; PRT; 118 AA.
AC Q9DF22;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE Actin (Fragment).
OS Scyliorhinus torazame (Cloudy catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carchariniiformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=75743;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cartilage;
RA Kim J.T., Kim M.S., Jang E.R., Kim Y.J., Kim K.W.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF305690; AAG22088.1; -.
DR HSP; P02568; IQ25.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 13380 MW; 9EE39214470C9ACS CRC64;

Query Match 100.0%; Score 81; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTMYPGIADRMQK 15
Db 66 GGTMYPGIADRMQK 80
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 62.4 Seconds
(without alignments)
92.971 Million cell updates/sec

Title: US-09-423-351C-5

Perfect score: 81

Sequence: 1 PRHQGVVMVGMQKDS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	15	2	Aaw92531 Beta-acti
2	81	100.0	105	5	Abp42469 Human ova
3	81	100.0	157	4	Abb66853 Drosophil
4	81	100.0	201	5	Abp43176 Human ova
5	81	100.0	204	5	Abp43016 Human ova
6	81	100.0	207	4	Abg15288 Novel hum
7	81	100.0	219	8	Abc058422 Human gen
8	81	100.0	310	8	Adr38362 pigA3Cy3G
9	81	100.0	342	7	Adm05323 Human pro
10	81	100.0	374	3	Aay78101 Misgurnus
11	81	100.0	374	3	Abi12985 Human bet
12	81	100.0	375	1	Aap61532 Sequence
13	81	100.0	375	2	Aar50328 Drug resi
14	81	100.0	375	3	Aab15017 Posttrans
15	81	100.0	375	3	Aay94569 Human car
16	81	100.0	375	3	Abi15016 Posttrans
17	81	100.0	375	5	Abb77395 Human act
18	81	100.0	375	6	Abf64271 Angiogene
19	81	100.0	375	6	Abm04830 Rat cytop
20	81	100.0	375	7	Abd85212 Rat actin
21	81	100.0	375	7	Adb61174 Rat Prote
22	81	100.0	375	7	Adf30525 Rat angio
23	81	100.0	375	7	Adi63062 Human apo
24	81	100.0	375	7	Adi62970 Human apo
25	81	100.0	375	7	Adi63040 Human apo

ALIGNMENTS

RESULT 1

AAW92531
ID AAW92531 standard; peptide; 15 AA.

XX AC AAW92531;

DT 26-APR-1999 (first entry)

XX DE Beta-actin reference peptide substrate #5.

KW Peptide substrate; CCT; eukaryotic type II chaperonin complex; cyclin;
KW binding agent; substrate-binding site; SBS; substrate folding; actin;
KW tubulin; treatment; cancer; anticancer drug; viral infection; screening;
KW reduced toxicity.

XX OS Synthetic.

XX PN WO9853322-A1.

XX PD 26-NOV-1998.

XX PF 22-MAY-1998; 98WO-GB001485.

XX PR 23-MAY-1997; 97GB-00010762.

XX PA (CANC-) INST CANCER RES ROYAL CANCER HOSPITAL.

XX PI Willison K, Hynes G, Liou AK;

XX DR WPI; 1999-070162/06.

XX PT Identifying specific binding agents for substrate binding site in CCT
XX chaperonin complex - also new peptide binding agents and their mimetics,
XX chaperonin complex containing a specific CCT binding site, used for treating
XX cancer.

XX PS Disclosure; Fig 10; 97pp; English.

XX CC This invention describes a method which uses the CCT (eukaryotic type II
XX chaperonin) complex or part of it, for identifying a binding agent that
XX can occupy a substrate-binding site (SBS) on the CCT complex. By binding
XX to the CCT complex, the binding agents block an SBS so that biological
XX activity of the CCT complex is affected, particularly its ability to fold
XX substrates such as actin, tubulin and cyclin. The binding agents are
XX useful for treatment of cancer, particularly when used in combination
XX with an anticancer drug, or viral infections. Nucleic acid fragments are
XX used to screen for agents, e.g. binding agents that modulate interaction
XX between the CCT complex and a protein that is to be folded. The binding

ADL13002 Human ste
ADJ78489 Actin pro
ADL14103 Human ear
ADP04899 Sea squir
ADP12391 Protein e
ADQ26098 Gamma 1 a
ABO84772 Human can
ABm80841 Tumour-as
ADn23274 Bacterial
ADs88828 Amino aci
ADs88825 Amino aci
ADs88826 Amino aci
ADs88827 Amino aci
AAw19799 Gamma-smo
Abb58162 Drosophil
Abb61322 Drosophil
Abb60354 Drosophil
ABb64853 Drosophil
ABr62327 Pacific w
ADn03845 Antipsori

CC agents may target cells that are actively synthesising tubulin etc.
 CC (unlike known microtubule-stabilising agents that affect all cells), so
 CC should have reduced toxicity for normal cells. AM92527-W92541 are
 CC peptide substrates used in the method of the invention

XX Sequence 15 AA;

Query Match 100.0%; Score 81; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.8e-07; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0;

QY 1 PRHQGVWVGWGQKDS 15
 |||||
 Db 1 PRHQGVWVGWGQKDS 15

RESULT 2

ABP42469
 ID ABP42469 standard; protein; 105 AA.

XX AC ABP42469;

XX DT 22-AUG-2002 (first entry)

XX DE Human ovarian antigen HOCQ94, SEQ ID NO:3601.

XX KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive.

XX OS Homo sapiens.

XX PN WO200200677-A1.

XX PD 03-JAN-2002.

XX PF 07-JUN-2001; 2001WO-US018569.

XX PR 07-JUN-2000; 2000US-0209467P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Birse CE, Rosen CA;

XX DR WPI; 2002-147878/19.

XX DR N-PSDB; ABQ55546.

XX PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 PT cancer), immune disorders, cardiovascular disorders and neurological
 PT diseases.

XX PS Claim 11; SEQ ID NO 3601; 2922pp; English.

XX CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovary and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine

CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 105 AA;

Query Match 100.0%; Score 81; DB 5; Length 105;
 Best Local Similarity 100.0%; Pred. No. 2.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRHQGVWVGWGQKDS 15

Db 39 PRHQGVWVGWGQKDS 53

RESULT 3

ABB66853

ID ABB66853 standard; protein; 157 AA.

XX AC ABB66853;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster polypeptide SEQ ID NO 27351.

XX KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.

XX OS Drosophila melanogaster.

XX PN WO200171042-A2.

XX PD 27-SEP-2001.

XX PF 23-MAR-2001; 2001WO-US009231.

XX PR 23-MAR-2000; 2000US-0191637P.

XX PR 11-JUL-2000; 2000US-00614150.

XX PA (PEKE) PE CORP NY.

XX PI Venter JC, Adams M, Li PWD, Myers EW;

XX DR WPI; 2001-656860/75.

XX DR N-PSDB; ABL10956.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.

XX PS Disclosure; SEQ ID NO 27351; 21pp + Sequence Listing; English.

XX CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-

CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 157 AA;
 SQ
 Query Match 100.0%; Score 81; DB 4; Length 157;
 Best Local Similarity 100.0%; Pred. No. 3.5e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 PRHQGVVMGQKDS 15
 Db 39 PRHQGVVMGQKDS 53
 RESULT 4
 ABP43176
 ID ABP43176 standard; protein; 201 AA.
 XX
 AC ABP43176;
 XX
 DT 22-AUG-2002 (first entry)
 XX
 DE Human ovarian antigen HVQCQ49, SEQ ID NO:4308.
 XX
 DE Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive.
 XX
 OS Homo sapiens.
 XX
 PN WO200200677-A1.
 XX
 PD 03-JAN-2002.
 XX
 PF 07-JUN-2001; 2001WO-US018569.
 XX
 PR 07-JUN-2000; 2000US-0209467P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Birse CE, Rosen CA;
 XX
 DR WPI; 2002-147878/19.
 DR N-PSDB; ABQ56253.
 XX
 PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 PT cancer), immune disorders, cardiovascular disorders and neurological
 PT diseases.
 XX
 PS Claim 11; SEQ ID NO 4308; 2922pp; English.
 XX
 CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovary and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic

CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 201 AA;
 Query Match 100.0%; Score 81; DB 5; Length 201;
 Best Local Similarity 100.0%; Pred. No. 4.5e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 PRHQGVVMGQKDS 15
 Db 55 PRHQGVVMGQKDS 69
 RESULT 5
 ABP43016
 ID ABP43016 standard; protein; 204 AA.
 XX
 AC ABP43016;
 XX
 DT 22-AUG-2002 (first entry)
 XX
 DE Human ovarian antigen HSPSB24, SEQ ID NO:4148.
 XX
 DE Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive.
 XX
 OS Homo sapiens.
 XX
 PN WO200200677-A1.
 XX
 PD 03-JAN-2002.
 XX
 PF 07-JUN-2001; 2001WO-US018569.
 XX
 PR 07-JUN-2000; 2000US-0209467P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Birse CE, Rosen CA;
 XX
 DR WPI; 2002-147878/19.
 DR N-PSDB; ABQ56093.
 XX
 PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 PT cancer), immune disorders, cardiovascular disorders and neurological
 PT diseases.
 XX
 PS Claim 11; SEQ ID NO 4148; 2922pp; English.
 XX

CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (AB054131-AB056305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovary and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 204 AA;

Query Match 100.0%; Score 81; DB 5; Length 204;
 Best Local Similarity 100.0%; Pred. No. 4.6e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PRHQGVVMVGMGQKDS 15
 |||||
 Db 58 PRHQGVVMVGMGQKDS 72

RESULT 6

ABG15288
 ID ABG15288 standard; protein; 207 AA.

XX AC ABG15288;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #15279.

XX DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX OS WO200175067-A2.

XX PN 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX XX (HYSE-) HYSEQ INC.

XX XX Drmanac RT, Liu C, Tang YT;

XX XX WPI; 2001-639362/73.

XX DR N-PSDB; AAS79475.

XX PT New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

XX Claim 20; SEQ ID NO 45647; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activities. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 207 AA;

Query Match 100.0%; Score 81; DB 4; Length 207;

Best Local Similarity 100.0%; Pred. No. 4.7e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PRHQGVVMVGMGQKDS 15

|||||

Db 65 PRHQGVVMVGMGQKDS 79

RESULT 7

ABO58422
 ID ABO58422 standard; protein; 219 AA.

XX AC ABO58422;

XX DT 29-JUL-2004 (first entry)

XX DE Human genome derived single exon protein #4656.

XX DE Human; gene expression; single exon probe; microarray;
 KW alternative splicing event; genomic alteration.

XX OS Homo sapiens.

XX OS US2003194704-A1.

XX PN 16-OCT-2003.

XX PF 03-APR-2002; 2002US-00029386.

XX PR 03-APR-2002; 2002US-00029386.

XX XX (PENN/) PENN S G.

XX PA (RANK/) RANK D R.

XX PA (HANZ/) HANZEL D K.

XX XX Penn SG, Rank DR, Hanzel DK;

XX XX WPI; 2004-119264/12.

XX PT New human genome-derived single exon nucleic acid probes useful for human
 PT gene expression analysis, for identifying or characterizing alternative
 PT splicing events, for assessing genomic alterations or as tools for

PT surveying tissues.

PS Claim 45; SEQ ID NO 32056; 80pp; English.

XX The invention relates to a nucleic acid probe for measuring human gene
 CC expression, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that
 CC hybridises under high stringency conditions to a nucleic acid molecule
 CC expressed in human cells or tissues. Also included are a spatially-
 CC addressable set of single exon nucleic acid probes for measuring human
 CC gene expression (comprising a plurality of single exon nucleic acid
 CC probes cited above, where each of the plurality of probes is separately
 CC and addressably isolatable or amplifiable from the plurality), a single
 CC exon microarray for measuring human gene expression, a method of
 CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC methods of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing
 CC human gene expression data by subsequence, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above. The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterising
 CC alternative splicing events, in detecting and characterising gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe protein of the invention. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docID=20030194704

XX Sequence 219 AA;

Query Match 100.0%; Score 81; DB 8; Length 219;
 Best Local Similarity 100.0%; Pred. No. 5e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PRHQGVVMVGQKDS 15
 |||||
 Db 69 PRHQGVVMVGQKDS 83

RESULT 8
 ADR38362
 ID ADR38362 standard; protein; 310 AA.

XX ADR38362;

XX 18-NOV-2004 (first entry)

XX pigA3Cy3GFP plasmid protein product (Cycle3 GFP under an actin promoter).
 DE piggyBac; transposon; transposase; gene transfer; plasmid; Cycle3 GFP;
 KW actin promoter.

XX Bombyx mori.
 OS Synthetic.
 OS Unidentified.

XX Key Location/Qualifiers
 FH Misc-difference 20
 FT /note= "Encoded by GCC"

XX JP2004236642-A.

XX 26-AUG-2004.
 PD 10-FEB-2003; 2003JP-00032306.
 XX 10-FEB-2003; 2003JP-00032306.
 PR 10-FEB-2003; 2003JP-00032306.
 XX (TORA) TORAY IND INC.

XX WPI; 2004-608233/59.
 DR N-PSDB; ADR38361.

XX Introducing foreign gene into insect cell, involves introducing DNA
 XX having foreign gene integrated between inverted repeat sequences of
 XX piggyBac transposon and piggyBac transposase that acts on inverted repeat
 XX sequence.

XX Disclosure; Page; 25pp; Japanese.

XX This invention relates to a novel method for introducing a foreign gene
 CC into an insect cell. Specifically, it refers to a foreign gene occurring
 CC between inverted repeat sequences of a piggyBac transposon and using a
 CC piggyBac transposase for gene transfer to give a high recombinant
 CC efficiency. The present invention describes the insect cell as that of
 CC Lepidoptera insect origin, preferably it is the silk worm Bombyx mori,
 CC and stable integration occurs into the genome of this insect using the
 CC transposase enzyme. In particular, this gene transfer method uses the
 CC plasmid pigA3Cy3GFP which contains a Cycle3 GFP gene expressed under a
 CC silk worm actin promoter (A3 promoter) between a pair of inverted repeat
 CC sequences of the transposon piggyBac. This polypeptide sequence is the
 CC protein product from the pigA3Cy3GFP plasmid DNA that represents the
 CC silkworm actin promoter controlling expression of the Cycle3 GFP gene
 CC given in an exemplification of the invention. NOTE: This sequence is
 CC given as an embedded protein in the sequence listing and is not referred
 CC to further within the specification.

XX Sequence 310 AA;

Query Match 100.0%; Score 81; DB 8; Length 310;
 Best Local Similarity 100.0%; Pred. No. 7.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PRHQGVVMVGQKDS 15
 |||||
 Db 39 PRHQGVVMVGQKDS 53

RESULT 9
 ADM05323
 ID ADM05323 standard; protein; 342 AA.

XX ADM05323;

XX 20-MAY-2004 (first entry)

XX Human protein of the invention SEQ ID NO:4008.

XX human; gene therapy; diagnostic marker; pharmaceutical.

XX Homo sapiens.

XX EPI347046-A1.

XX 24-SEP-2003.

XX 12-APR-2002; 2002EP-00008400.

XX 22-MAR-2002; 2002JP-00137785.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 XX Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;

PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
 XX WPI; 2003-723558/69.
 XX N-PSDB; ADM02880.
 XX New polynucleotides and polypeptides are useful in gene therapy, for
 PT developing a diagnostic marker or medicines for regulating their
 PT expression and activity, or as a target of gene therapy.
 XX Claim 1; SEQ ID NO 4008; 305pp; English.
 XX The invention relates to a novel human polynucleotide and the encoded
 CC polypeptide. A polynucleotide of the invention may have a use in gene
 CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
 CC as a primer for synthesizing the polynucleotide or as a probe for
 CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
 CC useful in gene therapy, for developing a diagnostic marker or medicines
 CC for regulating their expression and activity, or as a target of gene
 CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
 CC are useful as pharmaceutical agents. The present sequence represents a
 CC protein sequence of the invention.
 XX SQ Sequence 342 AA;
 Query Match 100.0%; Score 81; DB 7; Length 342;
 Best Local Similarity 100.0%; Pred. No. 8e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 PRHQGVVMVGQKDS 15
 Db 40 PRHQGVVMVGQKDS 54
 RESULT 10
 AAY78101
 ID AAY78101 standard; protein; 374 AA.
 XX AAY78101;
 AC AAY78101;
 XX 27-APR-2000 (first entry)
 DT Misgurnus mizolepis beta actin.
 DE Growth hormone; beta actin; controlling site; fish; breeding.
 XX Misgurnus mizolepis.
 OS Misgurnus mizolepis.
 XX JP2000004889-A.
 PN 11-JAN-2000.
 PD 01-JUN-1999; 95JP-00154346.
 XX 01-JUN-1999; 98KR-00020255.
 PR 23-JUL-1998; 98KR-00029701.
 XX (KIMD/) KIM D S.
 PA (KIMC/) KIM C G.
 PA (NOHJ/) NOH J G.
 PA (CHOK/) CHO K N.
 PA (NAMY/) NAM Y G.
 XX Cho KN, Kim CG, Kim DS, Nam YG, Noh JG;
 PI WPI; 2000-140126/13.
 XX N-PSDB; AAZ88225.
 XX A Misgurnus mizolepis growth hormone expression vector - containing DNA
 PT encoding a beta-actin gene.
 XX Claim 1; Page 16-20; 30pp; Japanese.
 XX The present invention describes a Misgurnus mizolepis growth hormone

CC expression vector. Also described is the DNA sequence given in AAZ88225
 CC which contains the beta actin gene and beta actin gene controlling site
 CC of Misgurnus mizolepis. Also described are: (1) an expression vector
 CC containing a growth hormone gene and the beta actin gene controlling site
 CC of Misgurnus mizolepis; and (2) a method for the preparation of a high
 CC growth transformed Misgurnus mizolepis including a step of finely
 CC injecting the above expression vector to fertilised eggs of Misgurnus
 CC mizolepis and hatching them. The vector can be used for the expression of
 CC useful genes in a fish. The method can reduce the breeding period of
 CC Misgurnus mizolepis. The present sequence represents the Misgurnus
 CC mizolepis beta actin amino acid sequence
 XX SQ Sequence 374 AA;
 Query Match 100.0%; Score 81; DB 3; Length 374;
 Best Local Similarity 100.0%; Pred. No. 8.8e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 PRHQGVVMVGQKDS 15
 Db 38 PRHQGVVMVGQKDS 52
 RESULT 11
 AAB12985
 ID AAB12985 standard; protein; 374 AA.
 XX AAB12985;
 AC AAB12985;
 XX 29-NOV-2000 (first entry)
 DT Human beta-actin protein sequence.
 DE Beta actin; post translational modification; sickle cell anaemia;
 KW irreversibly sickled cell; ISC; treatment.
 XX Homo sapiens.
 OS US6087398-A.
 PN 11-JUL-2000.
 PD 01-MAR-1996; 96US-00609236.
 XX 14-AUG-1995; 95US-0002288P.
 PR (SALA-) SOUTH ALABAMA MEDICAL SCI FOUND.
 PA Goodman SR;
 PI WPI; 2000-498210/44.
 XX Treatment for sickle cell anemia comprises administering a reducing agent
 PT to inhibit and reverse sickled cell formation in blood.
 XX Example 17; Fig 5B; 53pp; English.
 XX This invention provides a treatment for sickle cell anaemia, which
 CC comprises administering a reducing agent. The treatment inhibits the
 CC formation of irreversibly sickled cells (ISC) and reverses ISC formation
 CC in the blood. The present sequence represents the human beta-actin
 CC protein. The sequence is used in the invention to demonstrate that a
 CC disulphide bridge is formed between cysteines 284 and 373 in ISC beta-
 CC actin as a post-translational modification. The reducing agent used in
 CC the treatment acts to correct this post-translational modification
 XX SQ Sequence 374 AA;
 Query Match 100.0%; Score 81; DB 3; Length 374;
 Best Local Similarity 100.0%; Pred. No. 8.8e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 PRHQGVVMVGQKDS 15


```
Db      37 PRHQGVVMGMGQKDS 51
|||||
RESULT 12
AAP61532
ID AAP61532 standard; protein; 375 AA.
XX
AC AAP61532;
XX
DT 25-MAR-2003 (revised)
DT 13-SEP-1991 (first entry)
XX
DE Sequence of beta-actin.
XX
KW Actin fibre; actin film; recombinant beta-actin.
XX
OS Homo sapiens.
XX
PN EP174608-A.
XX
PD 19-MAR-1986.
XX
PF 05-SEP-1985; 8SEP-00111225.
XX
PR 13-SEP-1984; 84US-00650958.
XX
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI Leavitt JC, Kedes LH, Gunning PW;
XX
DR WPI; 1986-077015/12.
DR N-PSDB; AAN60172.
XX
PT Beta-actin gene and regulatory elements - used for expression of
PT polypeptide(s) in mammalian host cells.
XX
PS Example; Page 23-24; 32pp; English.
XX
CC In the example, a beta-actin expression vector providing the beta- actin
CC promoter region, a polylinker and a polyadenylation signal was
CC constructed where the expression construct was present on a vector having
CC a bacterial origin of replication, as well as a marker for selection in a
CC mammalian host. (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 375 AA;
Query Match 100.0%; Score 81; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 8.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PRHQGVVMGMGQKDS 15
Db 38 PRHQGVVMGMGQKDS 52
|||||
RESULT 13
AAR50328
ID AAR50328 standard; protein; 375 AA.
XX
AC AAR50328;
XX
DT 12-OCT-1994 (first entry)
XX
DE Drug resistant structural protein.
XX
KW Drug resistant; structural gene; expression vector; selective; marker;
XX transformation; thymidine-kinase deleted cell.
XX
OS Homo sapiens.
XX
PN JP06038773-A.
XX

PD 15-FEB-1994.
XX
PF 31-JAN-1992; 92JP-00045939.
XX
PR 31-JAN-1992; 92JP-00045939.
XX
PA (TOYM ) TOYOBO KK.
XX
DR WPI; 1994-094836/12.
DR N-PSDB; AAQ44861.
XX
PT Expression vector contg. drug resistant marker gene - useful for
PT transformation of thymidine kinase-deleted human cells for high levels of
PT foreign protein prodn.
XX
PS Disclosure; Page 5-7; 7pp; Japanese.
XX
CC This sequence is encoded by a drug resistant structural gene which may be
CC used in the expression vector of the invention. This gene is used as the
CC selective marker in the vector. The resulting vector may be used to
CC transform a thymidine-kinase deleted cell allowing introduction of a
CC foreign structural gene. The transformed cell may be used to produce
CC large amounts of useful protein
XX
SQ Sequence 375 AA;
Query Match 100.0%; Score 81; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 8.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PRHQGVVMGMGQKDS 15
Db 38 PRHQGVVMGMGQKDS 52
|||||
RESULT 14
AAB15017
ID AAB15017 standard; protein; 375 AA.
XX
AC AAB15017;
XX
DT 07-DEC-2000 (first entry)
XX
DE Posttranslationally modified human cardiac actin mutant E361G.
XX
KW Cardiac actin; ACTC; human; gene therapy; IDC; chromosome 15q14;
KW idiopathic dilated cardiomyopathy; mutant; mutein.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 361
FT /note= "Wild-type Glu substituted by Gly"
XX
PN US6063576-A.
XX
PD 16-MAY-2000.
XX
PF 29-JUN-1998; 98US-00106217.
XX
PR 29-JUN-1998; 98US-00106217.
XX
PA (UTAH ) UNIV UTAH RES FOUND.
XX
PI Olson TM, Keating MT;
XX
DR WPI; 2000-375488/32.
DR N-PSDB; AAA73739.
XX
PT New cardiac actin gene comprising histidine to arginine or glycine to
PT glutamic acid substitution, useful in the diagnosis of diseases
PT associated with the mutation, specifically idiopathic dilated
```

PT cardiomyopathy.
 XX Claim 3; Page; 36pp; English.
 XX
 CC The present invention relates to human cardiac actin (ACTC). Genotypic
 CC analyses show that ACTC is linked to idiopathic dilated cardiomyopathy
 CC (IDC). The ACTC gene maps to chromosome 15q14. Six PCR primer pairs
 CC (AAA49020 to AAA49031) have been developed to allow analysis of the six
 CC exons of ACTC. Studies of two families with IDC showed the presence of
 CC two mutations, one in exon 5 and one in exon 6. The present sequence is a
 CC mutant of posttranslationally modified ACTC without the initial two
 CC residues. The mutation is a Glu to Gly mutation at position 361. The ACTC
 CC protein may be used in a variety of methods for drug screening and for
 CC rational drug design. The ACTC gene may be used to treat IDC by gene
 CC therapy. Analysis of the ACTC gene provides early identification of
 CC subjects likely to develop or who already have IDC. Note: The present
 CC sequence is not shown in the specification but is derived from the ACTC
 CC sequence described in AAY94569
 XX
 XX Sequence 375 AA;
 SQ
 Query Match 100.0%; Score 81; DB 3; Length 375;
 Best Local Similarity 100.0%; Pred. No. 8.8e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PRHOGVVMVGQKDS 15
 |||||
 DB 38 PRHOGVVMVGQKDS 52
 Search completed: April 8, 2005, 10:50:43
 Job time : 62.4 secs

CC one in exon 5 and one in exon 6. The mutations are G to A in codon 312
 CC (Arg312His) and A to G in codon 361 (Glu361Gly). The ACTC protein may be
 CC used in a variety of methods for drug screening and for rational drug
 CC design. The ACTC gene may be used to treat IDC by gene therapy. Analysis
 CC of the ACTC gene provides early identification of subjects likely to
 CC develop or who already have IDC
 XX
 XX Sequence 375 AA;
 SQ
 Query Match 100.0%; Score 81; DB 3; Length 375;
 Best Local Similarity 100.0%; Pred. No. 8.8e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PRHOGVVMVGQKDS 15
 |||||
 DB 38 PRHOGVVMVGQKDS 52
 Search completed: April 8, 2005, 10:50:43
 Job time : 62.4 secs

Query Match 100.0%; Score 81; DB 3; Length 375;
 Best Local Similarity 100.0%; Pred. No. 8.8e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PRHOGVVMVGQKDS 15
 |||||
 DB 38 PRHOGVVMVGQKDS 52

RESULT 15
 AAY94569
 ID AAY94569 standard; protein; 375 AA.
 XX
 AC AAY94569;
 XX
 DT 07-DEC-2000 (first entry)
 XX
 XX Human cardiac actin protein after posttranslational modification.
 DE
 XX Cardiac actin; ACTC; human; gene therapy; IDC; 15q14;
 KW idiopathic dilated cardiomyopathy.
 XX
 OS Homo sapiens.
 XX
 XX US6063576-A.
 FN
 XX 16-MAY-2000.
 PD
 XX 29-JUN-1998; 98US-00106217.
 XX
 XX 29-JUN-1998; 98US-00106217.
 PR
 XX (UTAH) UNIV UTAH RES FOUND.
 PA
 XX Olson TM, Keating MT;
 PI
 XX WPI; 2000-375488/32.
 XX
 DR N-PSDB; AAA49032.
 DR
 XX New cardiac actin gene comprising histidine to arginine or glycine to
 PT glutamic acid substitution, useful in the diagnosis of diseases
 PT associated with the mutation, specifically idiopathic dilated
 PT cardiomyopathy.
 PT
 PS Claim 3; Col 61-62; 36pp; English.
 XX
 XX The present sequence is human cardiac actin (ACTC) protein, without the
 CC initial Met-Cys which is posttranslationally removed. Genotypic analyses
 CC show that ACTC is linked to idiopathic dilated cardiomyopathy (IDC). The
 CC ACTC gene maps to chromosome 15q14. Six PCR primer pairs (AAA49020 to
 CC AAA49031) have been developed to allow analysis of the six exons of ACTC.
 CC Studies of two families with IDC showed the presence of two mutations,

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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:57 ; Search time 17.5333 Seconds
(without alignments)
63.863 Million cell updates/sec

Title: US-09-423-351C-5

Perfect score: 81

Sequence: 1 PRHQGVVMGMGXQDS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

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- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	81	100.0	374	3	US-08-609-236-6
2	81	100.0	374	3	US-09-306-446C-2
3	81	100.0	375	2	US-08-494-151-14
4	81	100.0	375	3	US-09-106-217-16
5	81	100.0	375	4	US-09-976-594-731
6	81	100.0	376	1	US-08-588-113-2
7	81	100.0	376	4	US-09-949-016-6100
8	81	100.0	377	3	US-09-106-217-2
9	81	100.0	377	4	US-09-919-172-33
10	81	100.0	377	4	US-09-917-254-53
11	81	100.0	386	4	US-09-949-016-7721
12	81	100.0	399	4	US-09-949-016-9424
13	81	100.0	402	4	US-09-949-016-10757
14	81	100.0	404	4	US-09-949-016-11313
15	80	98.8	377	4	US-09-248-796A-14109
16	77	95.1	20	3	US-08-505-250-17
17	77	95.1	20	3	US-08-505-250-17
18	76	93.8	71	4	US-09-621-976-6521
19	74	91.4	375	3	US-09-171-337A-7
20	74	91.4	375	3	US-09-171-337A-8
21	74	91.4	375	4	US-09-631-022-7
22	74	91.4	375	4	US-09-631-022-8
23	56	69.1	80	3	US-09-306-446C-4
24	48	59.3	371	1	US-08-261-206A-77
25	45	55.6	397	4	US-09-902-540-9949
26	43	53.1	72	4	US-09-252-991A-28861
27	43	53.1	843	4	US-09-252-991A-32609

28	41	50.6	543	4	US-09-252-991A-18055	Sequence 18055, A
29	40	49.4	211	4	US-09-252-991A-18464	Sequence 18464, A
30	40	49.4	832	4	US-09-540-236-3056	Sequence 3056, Ap
31	40	49.4	862	4	US-09-543-681A-6315	Sequence 6315, Ap
32	39	48.1	334	4	US-09-949-016-11006	Sequence 11006, A
33	39	48.1	338	4	US-09-252-991A-22180	Sequence 22180, A
34	39	48.1	453	4	US-09-252-991A-31634	Sequence 31634, A
35	39	48.1	817	4	US-09-252-991A-27609	Sequence 27609, A
36	38	46.9	120	4	US-09-765-815-3	Sequence 3, Appli
37	38	46.9	245	4	US-09-902-540-13736	Sequence 13736, A
38	38	46.9	266	4	US-09-270-767-44486	Sequence 44486, A
39	38	46.9	516	4	US-09-252-991A-17933	Sequence 17933, A
40	38	46.9	545	4	US-09-538-092-1297	Sequence 1297, A
41	38	46.9	652	1	US-08-765-081-6	Sequence 6, Appli
42	38	46.9	652	3	US-09-098-082-6	Sequence 6, Appli
43	38	46.9	957	4	US-09-252-991A-30672	Sequence 30672, A
44	37	45.7	62	4	US-09-248-796A-22522	Sequence 22522, A
45	37	45.7	66	4	US-09-543-681A-7224	Sequence 7224, Ap

ALIGNMENTS

RESULT 1
US-08-609-236-6
; Sequence 6, Application US/08609236
; Patent No. 6087398
; GENERAL INFORMATION:
; APPLICANT: Steven R. Goodman
; TITLE OF INVENTION: NO. 6087398el Sickie Cell Anemia Treatment
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McGregor & Adler, LLP
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,236
; FILING DATE: March 1, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/002,288
; FILING DATE: August 14, 1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Benjamin Aaron Adler, Ph.D.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5807
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6908
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374
; TYPE: Amino acid
; STRANDEDNESS:
; TOPOLOGY: Linear
; MOLECULE TYPE:
; DESCRIPTION: Protein
; HYPOTHETICAL: No
; ANTI-SENSE: No
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:

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; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
US-08-609-236-6

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Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRHQGVVMVGMGQKDS 15
Db 37 PRHQGVVMVGMGQKDS 51

RESULT 2
US-09-306-446C-2
; Sequence 2, Application US/09306446C
; Patent No. 6372959
; GENERAL INFORMATION:
; APPLICANT: KIM, Dong Soo
; APPLICANT: KIM, Chul Geun
; APPLICANT: NAM, Yoon Kwon
; APPLICANT: NOH, Jae Koo
; APPLICANT: CHO, Kyou Nam
; TITLE OF INVENTION: EXPRESSION VECTOR OF MUD LOACH GROWTH HORMONE GENE
; FILE REFERENCE: P06344US/0/BAS
; CURRENT APPLICATION NUMBER: US/09/306,446C
; CURRENT FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: KR 98/20255
; PRIOR FILING DATE: 1998-06-01
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Misgurnus mizolepus
US-09-306-446C-2

Query Match      100.0%; Score 81; DB 3; Length 374;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRHQGVVMVGMGQKDS 15
Db 38 PRHQGVVMVGMGQKDS 52

RESULT 3
US-08-494-151-14
; Sequence 14, Application US/08494151
; Patent No. 5840528
; GENERAL INFORMATION:
; APPLICANT: Van Ooyen, Albert Johannes Joseph
; TITLE OF INVENTION: Transformation of Phaffia rhodozyma
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 23-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muraahige, Kate H.
; REGISTRATION NUMBER: 29,959

; REFERENCE/DOCKET NUMBER: 24615-20039.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-494-151-14

Query Match      100.0%; Score 81; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRHQGVVMVGMGQKDS 15
Db 38 PRHQGVVMVGMGQKDS 52

RESULT 4
US-09-106-217-16
; Sequence 16, Application US/09106217
; Patent No. 6063576
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Olson, Timothy M.
; TITLE OF INVENTION: Actin Mutations in Dilated
; TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; STREET: Tower
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Save, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 2323-125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-106-217-16

Query Match      100.0%; Score 81; DB 3; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRHQGVVMVGMGQKDS 15
Db 38 PRHQGVVMVGMGQKDS 52
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RESULT 5

US-09-976-594-731
; Sequence 731, Application US/09976594
; Patent No. 6673549

GENERAL INFORMATION:

APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
SEQ ID NO 731
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673549 1837317CD1
US-09-976-594-731

Query Match 100.0%; Score 81; DB 4; Length 375;

Best Local Similarity 100.0%; Pred. No. 1.9e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVMGQKDS 15

|||||

Db 38 PRHQGVVMGQKDS 52

RESULT 6

US-08-588-113-2
; Sequence 2, Application US/08588113
; Patent No. 5710003

GENERAL INFORMATION:

APPLICANT: McHugh, Kirk M.
TITLE OF INVENTION: DIAGNOSTIC TEST FOR DETERMINING
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 5710003ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,113

FILING DATE:

CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Ralph, Rebecca L.
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: TLU-1652
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-588-113-2

Query Match

100.0%; Score 81; DB 1; Length 376;

Best Local Similarity 100.0%; Pred. No. 2e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVMGQKDS 15

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Db 39 PRHQGVVMGQKDS 53

RESULT 7

US-09-949-016-6100

; Sequence 6100, Application US/09949016

; Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6100
LENGTH: 376
TYPE: PRT
ORGANISM: Human
US-09-949-016-6100

Query Match

100.0%; Score 81; DB 4; Length 376;

Best Local Similarity 100.0%; Pred. No. 2e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVMGQKDS 15

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Db 39 PRHQGVVMGQKDS 53

RESULT 8

US-09-106-217-2

; Sequence 2, Application US/09106217

; Patent No. 6063576

GENERAL INFORMATION:

APPLICANT: Keating, Mark T.
APPLICANT: Olson, Timothy M.
TITLE OF INVENTION: Actin Mutations in Dilated
TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
STREET: 555 Thirteenth Street, N.W., Suite 701 East
STREET: Tower
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/106,217
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.

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;
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 2323-125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-106-217-2

Query Match 100.0%; Score 81; DB 3; Length 377;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVMVGMGQKDS 15
Db 40 PRHQGVVMVGMGQKDS 54

RESULT 9
US-09-919-172-33
; Sequence 33, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 33
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 1709118CD1
US-09-919-172-33

Query Match 100.0%; Score 81; DB 4; Length 377;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVMVGMGQKDS 15
Db 40 PRHQGVVMVGMGQKDS 54

RESULT 10
US-09-917-254-53
; Sequence 53, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
; APPLICANT: Mutter, George
; APPLICANT: Baak, Jan
; TITLE OF INVENTION: Prognostic Classification of Breast Cancer
; FILE REFERENCE: B0801/7224(JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/222,093
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 53
; LENGTH: 377
; TYPE: PRT

; ORGANISM: Homo Sapiens
US-09-917-254-53

Query Match 100.0%; Score 81; DB 4; Length 377;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVMVGMGQKDS 15
Db 40 PRHQGVVMVGMGQKDS 54

RESULT 11
US-09-949-016-7721
; Sequence 7721, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7721
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7721

Query Match 100.0%; Score 81; DB 4; Length 386;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVMVGMGQKDS 15
Db 49 PRHQGVVMVGMGQKDS 63

RESULT 12
US-09-949-016-9424
; Sequence 9424, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9424
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9424

Query Match 100.0%; Score 81; DB 4; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHOGVMVGMGQKDS 15
Db 62 PRHOGVMVGMGQKDS 76

RESULT 13

US-09-949-016-10757
; Sequence 10757, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10757
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10757

Query Match 100.0%; Score 81; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHOGVMVGMGQKDS 15
Db 65 PRHOGVMVGMGQKDS 79

RESULT 14

US-09-949-016-11313
; Sequence 11313, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11313
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11313

Query Match 100.0%; Score 81; DB 4; Length 404;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHOGVMVGMGQKDS 15
Db 67 PRHOGVMVGMGQKDS 81

RESULT 15

US-09-248-796A-14109
; Sequence 14109, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 14109
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-14109

Query Match 98.8%; Score 80; DB 4; Length 377;
Best Local Similarity 93.3%; Pred. No. 3e-06;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHOGVMVGMGQKDS 15
Db 40 PRHOGVMVGMGQKDS 54

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Job time : 17.5333 secs

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OM protein - protein search, using sw model

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April 8, 2005, 10:53:18 ; Search time 42.6667 Seconds
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- 116.718 Million cell updates/sec

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Title: US-09-423-351C-5
Perfect score: 81
Sequence: 1 PRHOGVMVGMGOKDS

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 331997259 residues

Total number of hits satisfying chosen parameters: 1418010

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	81	100.0	105	15	US-10-264-049-3601
2	81	100.0	142	15	Sequence 3601, Ap
3	81	100.0	201	15	Sequence 184471, Ap
4	81	100.0	204	15	Sequence 4308, Ap
5	81	100.0	219	14	Sequence 4148, Ap
6	81	100.0	219	14	Sequence 56, Appl
7	81	100.0	342	15	Sequence 32056, A
8	81	100.0	371	16	Sequence 4008, Ap
9	81	100.0	375	14	Sequence 68, Appl
10	81	100.0	375	14	Sequence 93, Appl
11	81	100.0	375	15	Sequence 88, Appl
12	81	100.0	375	15	Sequence 5927, Ap
13	81	100.0	375	15	Sequence 94, Appl
					Sequence 82, Appl

Sequence 101, Appl
Sequence 33, Appl
Sequence 64, Appl
Sequence 4, Appl
Sequence 310, Appl
Sequence 63, Appl
Sequence 1436, Ap
Sequence 1786, Ap
Sequence 1, Appl
Sequence 2436, Ap
Sequence 161246,
Sequence 202833,
Sequence 35226, A
Sequence 47318, A
Sequence 280811,
Sequence 282905,
Sequence 42770, A
Sequence 162684,
Sequence 283333,
Sequence 179917,
Sequence 204240,
Sequence 45677, A
Sequence 46090, A
Sequence 52, Appl
Sequence 162093,
Sequence 162685,
Sequence 162686,
Sequence 222816,
Sequence 223492,
Sequence 283336,
Sequence 66124, A

ALIGNMENTS

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RESULT 1
US-10-264-049-3601
; Sequence 3601, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133PI
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 3601
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (103)
; OTHER INFORMATION: Xaa equals any of the twenty naturally
US-10-264-049-3601

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RESULT 2

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US-10-424-599-184471
; Sequence 184471, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 184471
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_137594C.1.pep
; US-10-424-599-184471

Query Match      100.0%; Score 81; DB 15; Length 142;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVMVGMGQKDS 15
Db 47 PRHQGVVMVGMGQKDS 61

RESULT 3
US-10-264-049-4308
; Sequence 4308, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4308
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (135)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; NAME/KEY: MISC FEATURE
; LOCATION: (136)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (140)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (143)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (144)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
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; LOCATION: (145)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (151)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (159)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
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; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (174)
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; NAME/KEY: MISC FEATURE
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; US-10-264-049-4308

Query Match      100.0%; Score 81; DB 15; Length 201;
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVMVGMGQKDS 15
Db 55 PRHQGVVMVGMGQKDS 69

RESULT 4
US-10-264-049-4148
; Sequence 4148, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4148
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-264-049-4148

Query Match      100.0%; Score 81; DB 15; Length 204;
Best Local Similarity 100.0%; Pred. No. 4.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVMVGMGQKDS 15
Db 58 PRHQGVVMVGMGQKDS 72

RESULT 5
US-10-002-631C-56
; Sequence 56, Application US/10002631C
; Publication No. US20030157486A1
; GENERAL INFORMATION:
; APPLICANT: Graff, Jonathon M.
; APPLICANT: Muenster, Matthew
; TITLE OF INVENTION: METHODS TO IDENTIFY SIGNAL SEQUENCES
; FILE REFERENCE: A34943 090495.0243
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; CURRENT APPLICATION NUMBER: US/10/002,631C
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/300,309
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-631C-56

Query Match      100.0%; Score 81; DB 14; Length 219;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 PRHQGVVMVGMGQKDS 15
Db      65 PRHQGVVMVGMGQKDS 79

RESULT 6
US-10-029-386-32056
; Sequence 32056, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32056
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC026717.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 16
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 23
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 6.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 20
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9.8
; OTHER INFORMATION: SWISSPROT HIT: P29751, EVALUATE 3.00e-94
US-10-029-386-32056

Query Match      100.0%; Score 81; DB 14; Length 219;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 PRHQGVVMVGMGQKDS 15
Db      69 PRHQGVVMVGMGQKDS 83

RESULT 7
US-10-108-260A-4008
; Sequence 4008, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 4008
; LENGTH: 342

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-4008

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Best Local Similarity 100.0%; Pred. No. 7.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 PRHQGVVMVGMGQKDS 15
Db      40 PRHQGVVMVGMGQKDS 54

RESULT 8
US-10-322-281-68
; Sequence 68, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-281-68

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Best Local Similarity 100.0%; Pred. No. 8.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 PRHQGVVMVGMGQKDS 15
Db      38 PRHQGVVMVGMGQKDS 52

RESULT 9
US-10-205-194-93
; Sequence 93, Application US/10205194
; Publication No. US20030134301A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pinnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018201
; CURRENT APPLICATION NUMBER: US/10/205,194
; CURRENT FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 93
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Rattus rattus
; FEATURE:
; OTHER INFORMATION: Cytoplasmic gamma isoform of actin
US-10-205-194-93

Query Match      100.0%; Score 81; DB 14; Length 375;
Best Local Similarity 100.0%; Pred. No. 8.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 PRHQGVVMVGMGQKDS 15

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Db          38 PRHQGVVMVGMGQKDS 52

RESULT 10
US-10-316-253-88
; Sequence 88, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-88

Query Match          100.0%; Score 81; DB 14; Length 375;
Best Local Similarity 100.0%; Pred. No. 8.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          38 PRHQGVVMVGMGQKDS 52

RESULT 11
US-10-369-493-5927
; Sequence 5927, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5927
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5927

Query Match          100.0%; Score 81; DB 15; Length 375;
Best Local Similarity 100.0%; Pred. No. 8.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 PRHQGVVMVGMGQKDS 15
           |||||
Db          38 PRHQGVVMVGMGQKDS 52

RESULT 12
US-10-205-331-94
; Sequence 94, Application US/10205331
; Publication No. US20040058326A1
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; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pinnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018199
; CURRENT APPLICATION NUMBER: US/10/205,331
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 94
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Cytoplasmic beta-actin
US-10-205-331-94

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Best Local Similarity 100.0%; Pred. No. 8.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 PRHQGVVMVGMGQKDS 15
           |||||
Db          38 PRHQGVVMVGMGQKDS 52

RESULT 13
US-10-260-708-82
; Sequence 82, Application US/10260708
; Publication No. US20040063101A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Lee, Sang-Yull
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: Human Sarcoma-Associated Antigens
; FILE REFERENCE: L00461/70138
; CURRENT APPLICATION NUMBER: US/10/260,708
; CURRENT FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 375
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-260-708-82

Query Match          100.0%; Score 81; DB 15; Length 375;
Best Local Similarity 100.0%; Pred. No. 8.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 PRHQGVVMVGMGQKDS 15
           |||||
Db          38 PRHQGVVMVGMGQKDS 52

RESULT 14
US-10-341-434-101
; Sequence 101, Application US/10341434
; Publication No. US20030215835A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
; FILE REFERENCE: 9U 204 205 R1
; CURRENT APPLICATION NUMBER: US/10/341,434
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/348,164
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 60/348,119
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; PRIOR FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-341-434-101
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Query Match      100.0%; Score 81; DB 15; Length 376;
Best Local Similarity 100.0%; Pred. No. 8.5e-06;
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Db      39 PRHQGVVMGQKDS 53
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RESULT 15
US-09-919-172-33
; Sequence 33, Application US/09919172
; Patent No. US20020119463A1
; GENERAL INFORMATION:
; APPLICANT: Farris, Mary
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 33
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020119463A1 1709118CD1
US-09-919-172-33
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Query Match      100.0%; Score 81; DB 9; Length 377;
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 PRHQGVVMGQKDS 15
      |||||
Db      40 PRHQGVVMGQKDS 54
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Job time : 43.6667 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 9.33333 Seconds
(without alignments)
154.634 Million cell updates/sec

Title: US-09-423-351C-5
Perfect score: 81
Sequence: 1 PRHQGVVMGMGQKDS 15
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79: *
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	100.0	86	C43616	actin beta, cytosolic
2	81	100.0	137	A28258	actin 5C, fruit fly
3	81	100.0	158	D19465	alpha-cardiac actin
4	81	100.0	213	A61043	actin CA15 - sea s
5	81	100.0	308	A03000	actin 3 - fruit fl
6	81	100.0	328	S05430	actin beta - grass
7	81	100.0	349	B25819	actin, fetal skele
8	81	100.0	362	A26559	actin type 5, cyto
9	81	100.0	374	ATBOB	actin beta - bovin
10	81	100.0	374	ATBOG	actin gamma - bovi
11	81	100.0	374	JC5818	gamma-actin - huma
12	81	100.0	375	ATBOSM	actin, aortic smoo
13	81	100.0	375	ATRB	actin, skeletal mu
14	81	100.0	375	ATRTC	actin beta - rat
15	81	100.0	375	A48324	actin beta, cytosk
16	81	100.0	375	ATCHB	actin beta - chick
17	81	100.0	375	ATHUB	actin beta - human
18	81	100.0	375	ATHUG	actin gamma 1 - hu
19	81	100.0	375	ATMSB	actin beta - mouse
20	81	100.0	375	ATMSG	actin gamma - mous
21	81	100.0	375	ATRB	actin beta, non-mu
22	81	100.0	375	S11222	actin gamma, cytos
23	81	100.0	375	T25272	hypothetical prote
24	81	100.0	375	S71125	actin beta-2, cyto
25	81	100.0	375	S71124	actin beta-1, cyto
26	81	100.0	375	S71126	actin beta, cytosk
27	81	100.0	375	A55001	actin beta - goose
28	81	100.0	375	A54728	actin alpha, cardi
29	81	100.0	375	S42103	actin - Puccinia g

ALIGNMENTS

RESULT 1

C43616
actin beta, cytosolic - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
C:Accession: C43616
R:Paterson, B.M.; Eldridge, J.D.
Science 224, 1436-1438, 1984
A:Title: alpha-Cardiac actin is the major sarcomeric isoform expressed in embryonic avia
A:Reference number: A43616; MUID:84223949; PMID:6729461
A:Accession: C43616
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-86 <PAT>
A:Cross-references: UNIPROT:Q90736; GB:K02173; NID:G211054; PIDN:AAA98513.1; PID:G211055
C:Superfamily: actin
C:Keywords: cytosol; methylated amino acid
F:73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 81; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVMGMGQKDS 15
Db 38 PRHQGVVMGMGQKDS 52

RESULT 2

A28258
actin 5C - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C:Accession: A28258
R:Vigoreaux, J.O.; Tobin, S.L.
Genes Dev. 1, 1161-1171, 1987
A:Title: Stage-specific selection of alternative transcriptional initiation sites from t
A:Reference number: A28258; MUID:88112795; PMID:3123314
A:Accession: A28258
A:Molecule type: mRNA
A:Residues: 1-137 <VIG>
A:Cross-references: UNIPROT:P10987
A:Note: the authors translated the codon GAG for residue 96 as Gly
C:Genetics:
A:Gene: FlyBase:Act5C
A:Cross-references: FlyBase:FBgn0000042
C:Superfamily: actin
C:Keywords: methylated amino acid
F:74/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 81; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 5.3e-07;

actin - Phaffia rh
actin gamma, cytos
actin gamma, smoot
actin 8 - fruit fl
actin CyI - sea ur
Actin-1A - nematod
actin 87E - fruit
actin - fruit fly
actin, cytosolic -
actin, muscle - st
actin 15A - sea ur
actin - sea urchin
actin gamma, enter
actin - Hydra atte
actin (clone gen3)
actin (clones Ia a

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVVGMGQKDS 15
| | | | | | | | | | | | | | | |
Db 39 PRHQGVVVGMGQKDS 53

RESULT 3

149465
A:Species: Drosophila melanogaster (fragments)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: A03000
R:Flyberg, E.A.; Bond, B.J.; Hershey, N.D.; Mixter, K.S.; Davidson, N.
Cell 24, 107-116, 1981
A:Title: The actin genes of Drosophila: protein coding regions are highly conserved but
A:Reference number: A03000; MUID:81210174; PMID:6263481
A:Accession: A03000
A:Molecule type: DNA
A:Residues: 1-158 <RES>
A:CROSS-references: UNIPROT:P02572
A:Note: there are 68 unsequenced residues between positions 160 and 161. Partial sequence
C:Note: the authors translated the codon GTT for residue 263 as Ile
C:Genetics:
A:Gene: FlyBase:Act42A
A:CROSS-references: FlyBase:FBgn0000043
A:Map position: 42A
C:Superfamily: actin
C:Keywords: methylated amino acid
F:74/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 81; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 6.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVVGMGQKDS 15
| | | | | | | | | | | | | | | |
Db 47 PRHQGVVVGMGQKDS 61

RESULT 4

A61043
actin CAL5 - sea squirt (Styela clava) (fragments)
C:Species: Styela clava
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: A61043
R:Beach, R.L.; Jeffery, W.R.
Dev. Genet. 11, 2-14, 1990
A:Title: Temporal and spatial expression of a cytoskeletal actin gene in the ascidian
A:Reference number: A61043; MUID:90298580; PMID:2361333
A:Accession: A61043
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-213 <BEA>
A:CROSS-references: UNIPROT:Q7M3V7
C:Comment: This sequence is expressed in cells undergoing rapid cell division.
C:Superfamily: actin
C:Keywords: cytoskeleton; methylated amino acid; mitosis; structural protein
F:73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 81; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 8.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVVGMGQKDS 15
| | | | | | | | | | | | | | | |
Db 38 PRHQGVVVGMGQKDS 52

RESULT 5

A03000

actin 3 - fruit fly (Drosophila melanogaster) (fragments)
C:Species: Drosophila melanogaster
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: A03000
R:Flyberg, E.A.; Bond, B.J.; Hershey, N.D.; Mixter, K.S.; Davidson, N.
Cell 24, 107-116, 1981
A:Title: The actin genes of Drosophila: protein coding regions are highly conserved but
A:Reference number: A03000; MUID:81210174; PMID:6263481
A:Accession: A03000
A:Molecule type: DNA
A:Residues: 1-308 <FYP>
A:CROSS-references: UNIPROT:P02572
A:Note: there are 68 unsequenced residues between positions 160 and 161. Partial sequence
C:Note: the authors translated the codon GTT for residue 263 as Ile
C:Genetics:
A:Gene: FlyBase:Act42A
A:CROSS-references: FlyBase:FBgn0000043
A:Map position: 42A
C:Superfamily: actin
C:Keywords: methylated amino acid
F:74/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 81; DB 2; Length 308;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVVGMGQKDS 15
| | | | | | | | | | | | | | | |
Db 39 PRHQGVVVGMGQKDS 53

RESULT 6

S05430
actin beta - grass carp
C:Species: Ctenopharyngodon idella (grass carp)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C:Accession: S05430
R:Liu, Z.; Zhu, Z.; Roberg, K.; Faras, A.J.; Guise, K.S.; Kapuscinski, A.R.; Hackett, P.F.
Nucleic Acids Res. 17, 5850, 1989
A:Title: The beta-actin gene of carp (Ctenopharyngodon idella).
A:Reference number: S05430; MUID:89345185; PMID:2762162
A:Accession: S05430
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-328 <LIU>
A:CROSS-references: UNIPROT:P83751; EMBL:M25013
C:Genetics:
A:Introns: 41/3; 121/3; 268/1
C:Superfamily: actin
C:Keywords: cytoskeleton; methylated amino acid
F:73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 81; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVVGMGQKDS 15
| | | | | | | | | | | | | | | |
Db 38 PRHQGVVVGMGQKDS 52

RESULT 7

B25819
actin, fetal skeletal/adult cardiac muscle - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 09-Jul-2004
C:Accession: B25819
R:Alonso, S.; Minty, A.; Bourlet, Y.; Buckingham, M.
J. Mol. Evol. 23, 11-22, 1986
A:Title: Comparison of three actin-coding sequences in the mouse; evolutionary relations
A:Reference number: A25819; MUID:86200234; PMID:3084797
A:Accession: B25819
A:Molecule type: mRNA

Query Match	100.0%	Score 81;	DB 1;	Length 374;
Best Local Similarity	100.0%;	pred. No. 1.5e-06;		
Matches 15:	Conservative	0;	Mismatches 0;	Indels 0;
				Gaps 0;

RESULT 12
ATBOSM
actin, aortic.smooth muscle - bovine
C/Spectes: Bos primigenius taurus (cattle)
C/Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 06-Sep-1996
C/Accession: A02997; S13480

A;Residues: 48-54;68-72;235-243 <STR>
A;Experimental source: skeletal muscle
R;Bertrand, R.; Derancourt, J.; Kasseab, R.
FEBS Lett. 345, 113-119, 1994
A;Title: The covalent maleimidebenzoyl-actin-myosin head complex. Cross-linking of the S
A;Reference number: S44393; MUID:94259162; PMID:8200441
A;Accession: S44393
A;Molecule type: protein
A;Residues: 48-64 <BER>
A;Experimental source: skeletal muscle
C;Superfamily: actin
C;Keywords: acetylated amino end; ATP binding; methylated amino acid; muscle contraction
F;1-375/Product: actin #status experimental <MAT>
F;1/Modified site: acetylated amino end (Asp) #status experimental
F;73/Modified site: 3'-methylhistidine (His) #status experimental

Query Match 100.0%; Score 81; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVVGMGQKDS 15
||| ||||| |||||
Db 38 PRHQGVVVGMGQKDS 52

RESULT 14
ATRTC
actin beta - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 22-Jun-1999
C;Accession: A38571; A02999
R;Nudel, U.; Zakut, R.; Shani, M.; Neuman, S.; Levy, Z.; Yaffe, D.
Nucleic Acids Res. 11, 1759-1771, 1983
A;Title: The nucleotide sequence of the rat cytoplasmic beta-actin gene.
A;Reference number: A38571; MUID:83168920; PMID:6300777
A;Accession: A38571
A;Molecule type: DNA
A;Residues: 1-375 <NUD>
A;Cross-references: GB:J00691; NID:G202653; PIDN:AAA40657.1; PID:G202654
C;Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
C;Genetics:
A;Introns: 41/3; 121/3; 268/1; 328/3
C;Superfamily: actin
C;Keywords: cell motility; cytoskeleton; methylated amino acid; microfilament; mitosis;
F;2-375/Product: actin beta #status predicted <MAT>
F;73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 81; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVVGMGQKDS 15
||| ||||| |||||
Db 38 PRHQGVVVGMGQKDS 52

RESULT 15
A48324
actin beta, cytoskeletal - common carp
C;Species: Cyprinus carpio (common carp)
C;Date: 03-Feb-1994 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
C;Accession: A48324
R;Liu, Z.; Zhu, Z.; Roberg, K.; Faras, A.; Guise, K.; Kapuscinski, A.R.; Hackett, P.B.
DNA Seq. 1, 125-136, 1990
A;Title: Isolation and characterization of beta-actin gene of carp (Cyprinus carpio).
A;Reference number: A48324; MUID:92190540; PMID:2134183
A;Accession: A48324
A;Molecule type: DNA
A;Residues: 1-375 <LIU>
A;Cross-references: UNIPROT:P83750; GB:M24113; NID:G213041; PIDN:AAA68886.1; PID:G213042
A;Note: the authors translated the codon TTC for residue 21 as Pro, AAG for residue 50 as
7 as Pro
7: Note: the authors failed to translated the codon GGT for residue 42 as Gly

C;Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
 C;Genetics:
 A;Introns: 41/3; 121/3; 268/3; 328/3
 C;Superfamily: actin
 C;Keywords: acetylated amino end; cell motility; cytoskeleton; methylated amino acid; mi
 F;2-375/Product: actin beta, cytoskeletal #status predicted <MAR>
 F;2/Modified site: acetylated amino end (Asp) (in mature form) #status predicted
 F;73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 81; DB 1; Length 375;
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVVGQKDS 15
 |||||
 Db 38 PRHQGVVVGQKDS 52

Search completed: April 8, 2005, 10:53:05
 Job time : 9.3333 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 57.8667 Seconds
(without alignments)
132.739 Million cell updates/sec

Title: US-09-423-351C-5
Perfect score: 81
Sequence: 1 PRHQGVVMGQKDS 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	26	2	Q6Q298
2	81	100.0	53	2	Q6AW41
3	81	100.0	78	2	Q61375
4	81	100.0	78	2	Q61376
5	81	100.0	78	2	Q61377
6	81	100.0	79	2	Q95L83
7	81	100.0	80	2	Q9TTW4
8	81	100.0	86	2	Q90736
9	81	100.0	91	2	Q7ZZI1
10	81	100.0	96	2	Q86CV4
11	81	100.0	96	2	Q86FV7
12	81	100.0	99	2	Q9QZB4
13	81	100.0	100	2	Q86ZL0
14	81	100.0	104	2	Q86SB7
15	81	100.0	108	2	O18548
16	81	100.0	108	2	O18550
17	81	100.0	117	2	Q8T6P7
18	81	100.0	121	2	Q8JG71
19	81	100.0	121	2	Q78CQ1
20	81	100.0	129	2	Q6VBE4
21	81	100.0	130	2	Q93298
22	81	100.0	139	2	Q9DFK2
23	81	100.0	144	2	Q90YX9
24	81	100.0	150	2	Q804Y9
25	81	100.0	151	2	Q61274
26	81	100.0	151	2	Q9PSV5
27	81	100.0	158	2	Q61273
28	81	100.0	164	1	ACT_SPOLI
29	81	100.0	165	2	O17477
30	81	100.0	181	2	Q8JG41
31	81	100.0	181	2	Q8AWC8

32 81 100.0 181 2 Q8AWZ3
33 81 100.0 181 2 Q9DEU3
34 81 100.0 184 2 Q11209
35 81 100.0 186 2 Q8X190
36 81 100.0 189 2 Q8SPX4
37 81 100.0 191 2 Q64G12
38 81 100.0 198 2 Q6Y250
39 81 100.0 202 2 Q810R5
40 81 100.0 212 2 Q6ZYL2
41 81 100.0 213 2 Q7M3V7
42 81 100.0 225 2 Q64G13
43 81 100.0 236 2 Q6RXK3
44 81 100.0 254 2 Q7Z7J6
45 81 100.0 275 2 Q64I75

Q8awz3 argyrolelec
Q9deu3 scophthalmu
Q11209 canis fam1
Q8x190 paxillus in
Q8spx4 canis fam1
Q64g12 oxyuranus s
Q6y250 pagrus majo
Q810r5 mus musculu
Q6zyl2 arion lusit
Q7m3v7 styela clav
Q64g13 oxyuranus s
Q6rxk3 penaeus van
Q7z7j6 homo sapien
Q64i75 reticuliter

ALIGNMENTS

RESULT 1

Q6Q298 PRELIMINARY; PRT; 26 AA.
AC Q6Q298;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DE Beta actin (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Abomasum;
RA Shanmuganathan T., Hickford J.G.H., Savill M., Sykes A.R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY566300; AAS68014.1; -;
FT NON_TER 1
FT NON_TER 26
SQ SEQUENCE 26 AA; 2802 MW; C75DA20C92B36C4B CRC64;

Query Match 100.0%; Score 81; DB 2; Length 26;
Best Local Similarity 100.0%; Pred.No. 1.le-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVMGQKDS 15

|||||
Db 9 PRHQGVVMGQKDS 23

RESULT 2

Q6AW41 PRELIMINARY; PRT; 53 AA.
AC Q6AW41;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Cytoplasmic actin (fragment).
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Daizo; TISSUE=Silk gland;
RA Shiomi K., Kajiru Z., Nakagaki M., Yamashita O.;
RT "Baculovirus-mediated efficient gene transfer into the central nervous system of the silkworm, Bombyx mori.";
RL Nihon Sanehigaku Zasshi 72:149-155(2003).
RN [2]
RP SEQUENCE FROM N.A.

RC STRAIN=Daizo; TISSUE=Silk gland;
RA Shiom K.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB186491; BAD35130.1; -
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR NON_TER 53
FT SEQUENCE 53 AA; 5465 MW; 227AA84872EBA86 CRC64;

Query Match 100.0%; Score 81; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 21e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVGMGQKDS 15
| | | | | | | | | | | | | | | | | | | | | |
Db 39 PRHQGVVGMGQKDS 53

RESULT 3
O61375 PRELIMINARY; PRT; 78 AA.
ID O61375
AC O61375;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Actin 1 (Fragment).
GN Name=DpAct1;
OS Schmdtzea polychroa.
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC Paludicola; Dugesidae; Schmidtea.
OC NCBI_TaxID=50054;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9818684; PubMed=9518500; DOI=10.1093/nar/26.8.2031;
RA Fagotti A., Gabbiani G., Pascolini R., Neuville P.;
RT "Multiple isoform recovery (MIR)-PCR: a simple method for the
RT isolation of related mRNA isoforms";
RL Nucleic Acids Res. 26:2031-2033(1998).
CC -1- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells [By similarity].
CC -1- SIMILARITY: Belongs to the actin family.
DR EMBL; AF027161; AAC38981.1; -
DR HSPG; P02577; 1NM1.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
KW Structural protein.
FT NON_TER 78
FT SEQUENCE 78 AA; 8205 MW; 572BAB2698C24404 CRC64;

Query Match 100.0%; Score 81; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVGMGQKDS 15
| | | | | | | | | | | | | | | | | | | | | |
Db 39 PRHQGVVGMGQKDS 53

RESULT 4
O61376 PRELIMINARY; PRT; 78 AA.
ID O61376
AC O61376;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Actin 2 (Fragment).
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9818684; PubMed=9518500; DOI=10.1093/nar/26.8.2031;
RA Fagotti A., Gabbiani G., Pascolini R., Neuville P.;
RT "Multiple isoform recovery (MIR)-PCR: a simple method for the
RT isolation of related mRNA isoforms";
RL Nucleic Acids Res. 26:2031-2033(1998).
CC -1- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells [By similarity].
CC -1- SIMILARITY: Belongs to the actin family.
DR EMBL; AF027161; AAC38981.1; -
DR HSPG; P02577; 1NM1.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
KW Structural protein.
FT NON_TER 78
FT SEQUENCE 78 AA; 8205 MW; 572BAB2698C24404 CRC64;

Query Match 100.0%; Score 81; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVGMGQKDS 15
| | | | | | | | | | | | | | | | | | | | | |
Db 39 PRHQGVVGMGQKDS 53

RESULT 4
O61376 PRELIMINARY; PRT; 78 AA.
ID O61376
AC O61376;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Actin 2 (Fragment).
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9818684; PubMed=9518500; DOI=10.1093/nar/26.8.2031;
RA Fagotti A., Gabbiani G., Pascolini R., Neuville P.;
RT "Multiple isoform recovery (MIR)-PCR: a simple method for the
RT isolation of related mRNA isoforms";
RL Nucleic Acids Res. 26:2031-2033(1998).
CC -1- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells [By similarity].
CC -1- SIMILARITY: Belongs to the actin family.
DR EMBL; AF027161; AAC38981.1; -
DR HSPG; P02577; 1NM1.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
KW Structural protein.
FT NON_TER 78
FT SEQUENCE 78 AA; 8205 MW; 572BAB2698C24404 CRC64;

Query Match 100.0%; Score 81; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVGMGQKDS 15
| | | | | | | | | | | | | | | | | | | | | |
Db 39 PRHQGVVGMGQKDS 53

RESULT 4
O61376 PRELIMINARY; PRT; 78 AA.
ID O61376
AC O61376;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Actin 2 (Fragment).
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9818684; PubMed=9518500; DOI=10.1093/nar/26.8.2031;
RA Fagotti A., Gabbiani G., Pascolini R., Neuville P.;
RT "Multiple isoform recovery (MIR)-PCR: a simple method for the
RT isolation of related mRNA isoforms";
RL Nucleic Acids Res. 26:2031-2033(1998).
CC -1- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells [By similarity].
CC -1- SIMILARITY: Belongs to the actin family.
DR EMBL; AF027161; AAC38981.1; -
DR HSPG; P02577; 1NM1.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
KW Structural protein.
FT NON_TER 78
FT SEQUENCE 78 AA; 8205 MW; 572BAB2698C24404 CRC64;

Query Match 100.0%; Score 81; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVGMGQKDS 15
| | | | | | | | | | | | | | | | | | | | | |
Db 39 PRHQGVVGMGQKDS 53

RESULT 4
O61376 PRELIMINARY; PRT; 78 AA.
ID O61376
AC O61376;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Actin 2 (Fragment).
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9818684; PubMed=9518500; DOI=10.1093/nar/26.8.2031;
RA Fagotti A., Gabbiani G., Pascolini R., Neuville P.;
RT "Multiple isoform recovery (MIR)-PCR: a simple method for the
RT isolation of related mRNA isoforms";
RL Nucleic Acids Res. 26:2031-2033(1998).
CC -1- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells [By similarity].
CC -1- SIMILARITY: Belongs to the actin family.
DR EMBL; AF027161; AAC38981.1; -
DR HSPG; P02577; 1NM1.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
KW Structural protein.
FT NON_TER 78
FT SEQUENCE 78 AA; 8205 MW; 572BAB2698C24404 CRC64;

Query Match 100.0%; Score 81; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVGMGQKDS

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KW Structural protein.
FT NON TER 78
SQ SEQUENCE 78 AA; 8299 MW; B9DFP1108E4ADBOE CRC64;

Query Match 100.0%; Score 81; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVMVGMGQKDS 15
Db 39 PRHQGVVMVGMGQKDS 53

RESULT 6
Q95L83 PRELIMINARY; PRT; 79 AA.
AC Q95L83;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta-actin (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A. PubMed=1238084;
RX MEDLINE=22306422;
RA Wang D.-A., Du H., Jaggar J.H., Brindley D.N., Tigyí G.J.,
RA Watsky M.A.;
RT "Injury-elicited differential transcriptional regulation of
RT phospholipid growth factor receptors in the cornea.";
RL Am. J. Physiol. Cell Physiol. 283:C1646-C1654(2002).
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AF404278; AAL01885.1; -.
DR HSSP; P02577; INMI.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
KW Structural protein.
FT NON TER 79
SQ SEQUENCE 79 AA; 8420 MW; 05056E4E2AC092F8 CRC64;

Query Match 100.0%; Score 81; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVMVGMGQKDS 15
Db 40 PRHQGVVMVGMGQKDS 54

RESULT 7
Q9TTW4 PRELIMINARY; PRT; 80 AA.
AC Q9TTW4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta-actin (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
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OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA John S.J., Bildeau-Goeseels S.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AF191490; AAF05984.1; -.
DR HSSP; P02577; INMI.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
KW Structural protein.
FT NON TER 80
SQ SEQUENCE 80 AA; 9133 MW; 47354ABB7010668D CRC64;

Query Match 100.0%; Score 81; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVMVGMGQKDS 15
Db 4 PRHQGVVMVGMGQKDS 18

RESULT 8
Q90736 PRELIMINARY; PRT; 86 AA.
AC Q90736;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta-actin (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84223949; PubMed=6729461;
RA Paterson B.M., Eldridge J.D.;
RT "alpha-Cardiac actin is the major sarcomeric isoform expressed in
RT embryonic avian skeletal muscle.";
RL Science 224:1436-1438(1984).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; K02173; AAA98513.1; -.
DR PIR; C43616; C43616.
DR HSSP; P02577; INMI.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
KW Structural protein.
FT NON TER 86
SQ SEQUENCE 86 AA; 9351 MW; A55285196A328B6E CRC64;

Query Match 100.0%; Score 81; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 PRHQGVVMGQKDS 15
DB 38 PRHQGVVMGQKDS 52

RESULT 9
Q7ZZI1 PRELIMINARY; PRT; 91 AA.
AC Q7ZZI1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-actin (Fragment).
OS Salvelinus alpinus (Arctic char).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX NCBI_TaxID=8036;
RN [1]
RP SEQUENCE FROM N.A.
RA McGowan C., Davidson E.A., Davidson W.S.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
CC in all eukaryotic cells (By similarity).
DR EMBL; AY262761; AAP31127.1; -.
DR HSSP; P02577; INM1.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
KW Structural protein.
FT NON_TER 1
FT NON_TER 91
FT NON_TER 91
SQ SEQUENCE 91 AA; 10063 MW; 7118DB6663CD895C CRC64;

Query Match 100.0%; Score 81; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRHQGVVMGQKDS 15
DB 36 PRHQGVVMGQKDS 50

RESULT 10
Q86CV4 PRELIMINARY; PRT; 96 AA.
AC Q86CV4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Actin E2 (Fragment).
GN Drosophila novamexicana.
OS Drosophila novamexicana.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=47314;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=15010-1031.0;
RX MEDLINE=22480340; PubMed=12574518; DOI=10.1073/pnas.0336368100;
RA Wittkopp P.J., Williams B.L., Selegue J.E., Carroll S.B.;
RT "Drosophila pigmentation evolution: divergent genotypes underlying
RT convergent phenotypes.";
Proc. Natl. Acad. Sci. U.S.A. 100:1808-1813(2003).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AY165516; AAP12711.1; -.
DR HSSP; P02568; 1LCU.
DR FlyBase; FBgn0066281; Dame\ActE2.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
KW Structural protein.
FT NON_TER 96
FT NON_TER 96
SQ SEQUENCE 96 AA; 10610 MW; 1454B7D9DD3F3564 CRC64;

Query Match 100.0%; Score 81; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AY165541; AAP21565.1; -.
DR HSSP; P02568; 1LCU.
DR FlyBase; FBgn0066214; Dnov\ActE2.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
KW Structural protein.
FT NON_TER 96
FT NON_TER 96
SQ SEQUENCE 96 AA; 10610 MW; 1454B7D9DD3F3564 CRC64;

Query Match 100.0%; Score 81; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRHQGVVMGQKDS 15
DB 39 PRHQGVVMGQKDS 53

RESULT 11
Q86FV7 PRELIMINARY; PRT; 96 AA.
AC Q86FV7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Actin E2 (Fragment).
GN Name=ActE2;
OS Drosophila americana (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=40366;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=15010-0951.0;
RX MEDLINE=22480340; PubMed=12574518; DOI=10.1073/pnas.0336368100;
RA Wittkopp P.J., Williams B.L., Selegue J.E., Carroll S.B.;
RT "Drosophila pigmentation evolution: divergent genotypes underlying
RT convergent phenotypes.";
Proc. Natl. Acad. Sci. U.S.A. 100:1808-1813(2003).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AY165516; AAP12711.1; -.
DR HSSP; P02568; 1LCU.
DR FlyBase; FBgn0066281; Dame\ActE2.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
KW Structural protein.
FT NON_TER 96
FT NON_TER 96
SQ SEQUENCE 96 AA; 10610 MW; 1454B7D9DD3F3564 CRC64;

Query Match 100.0%; Score 81; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 PRHQGVVMVGQKDS 15
Db 39 PRHQGVVMVGQKDS 53

RESULT 12
Q9QZB4 PRELIMINARY; PRT; 99 AA.
AC Q9QZB4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytoplasmic actin (Fragment).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal gland;
RA Buelow H.E., Bernhardt R.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
CC EMBL; AF191277; AAF13923.1; -.
DR HSP; P02577; INM1.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
DR Structural protein.
KW NON TER 99
FT NON TER 99
SQ SEQUENCE 99 AA; 10973 MW; 0562B645E8DAF17B CRC64;

Query Match 100.0%; Score 81; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVMVGQKDS 15
Db 38 PRHQGVVMVGQKDS 52

RESULT 13
Q862L0 PRELIMINARY; PRT; 100 AA.
AC Q862L0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Similar to b-actin (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22544902; PubMed=12658628; DOI=10.1002/mrd.10292;
RA Ishiwata H., Katsuma S., Kizaki K., Patel O.V., Nakano H.,
RA Takahashi T., Inai K., Hirasawa A., Shiojima S., Ikawa H., Suzuki Y.,
RA Tsujimoto G., Izaike Y., Todoroki J., Hashizume K.;
RT "Characterization of gene expression profiles in early bovine
RT pregnancy using a custom cDNA microarray.";
RL Mol. Reprod. Dev. 65:9-18(2003).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
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CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
CC EMBL; AB098974; BAC56464.1; -.
DR HSP; P02568; IP8Z.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON TER 1
FT NON TER 100
SQ SEQUENCE 100 AA; 11601 MW; 0E14674471D0019D CRC64;

Query Match 100.0%; Score 81; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVMVGQKDS 15
Db 1 PRHQGVVMVGQKDS 15

RESULT 14
Q86SB7 PRELIMINARY; PRT; 104 AA.
AC Q86SB7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Actin (Fragment).
GN Name=ACT;
OS Gryllus bimaculatus (Two-spotted cricket).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC Gryllus.
OX NCBI_TaxID=6999;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang H., Shimmyo Y., Hirose A., Mito T., Inoue Y., Ohuchi H.,
RA Loukeris T.G., Noji S.;
RT "Extrachromosomal transposition of the transposable element Minos
RT occurs in embryos of the cricket Gryllus bimaculatus.";
RL Dev. Growth Differ. 0:0-0(2002).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
CC EMBL; AB087882; BAC55093.1; -.
DR HSP; P02577; INM1.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
KW Structural protein.
FT NON TER 104
SQ SEQUENCE 104 AA; 11511 MW; 332777A2B08669B0 CRC64;

Query Match 100.0%; Score 81; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVMVGQKDS 15
Db 39 PRHQGVVMVGQKDS 53
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RESULT 15
O18548
ID O18548 PRELIMINARY; PRT; 108 AA.
AC O18548;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Cytoplasmic actin lvc4 (Fragment).
GN Name=lvc4;
OS Lytechinus variegatus (Sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Temnopleuroidea; Toxopneustidae;
OC Lytechinus.
OX NCBI_TaxID=7654;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97333945; PubMed=9190067;
RA Kissinger J.C., Hahn J.H., Raff R.A.;
RT "Rapid evolution in a conserved gene family. Evolution of the actin
RL gene family in the sea urchin genus Helicodaris and related genera."
RL Mol. Biol. Evol. 14:654-665 (1997).
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; U82542; AAB66299.1; -.
DR HSSP; P10983; 1D4X.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS 1; 1.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 12094 MW; F670CB8A6CBD3AEA CRC64;

Query Match 100.0%; Score 81; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRHQGVVVGQKDS 15
Db 25 PRHQGVVVGQKDS 39

```

Search completed: April 8, 2005, 12:03:08
 Job time : 57.8667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 62.4 Seconds
(without alignments)
92.971 Million cell updates/sec

Title: US-09-423-351C-6
Perfect score: 74
Sequence: 1 TFTPMPVAVIAQAVL 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	15	2	Aaw92532 Beta-acti
2	74	100.0	97	4	Aam13687 Peptide #
3	74	100.0	97	4	Abb32618 Peptide #
4	74	100.0	97	4	Aam26087 Peptide #
5	74	100.0	97	4	Abb27467 Human pep
6	74	100.0	97	4	Abb18116 Protein #
7	74	100.0	97	4	Aam65825 Human bon
8	74	100.0	97	4	Aam53448 Human bra
9	74	100.0	97	4	Abg47471 Human liv
10	74	100.0	97	4	Aam01437 Peptide #
11	74	100.0	97	5	Abg35459 Human pep
12	74	100.0	137	4	Aau33076 Novel hum
13	74	100.0	150	4	Abg15101 Novel hum
14	74	100.0	166	4	Abg26869 Novel hum
15	74	100.0	168	5	Abp42912 Human ova
16	74	100.0	204	5	Abp43016 Human ova
17	74	100.0	239	7	Abg31206 Human dia
18	74	100.0	274	6	Abu70549 Human adi
19	74	100.0	276	3	Aag50947 Arabidops
20	74	100.0	277	3	Aag05115 Arabidops
21	74	100.0	294	7	Adi63068 Human apo
22	74	100.0	304	3	Aag50946 Arabidops
23	74	100.0	305	3	Aag05114 Arabidops
24	74	100.0	321	3	Aag50945 Arabidops
25	74	100.0	322	3	Aag05113 Arabidops

ALIGNMENTS

RESULT 1
Aaw92532
ID Aaw92532 standard; peptide; 15 AA.

XX AC Aaw92532;
XX AC
DT 26-APR-1999 (first entry)
DE Beta-actin reference peptide substrate #6.

XX Peptide substrate; CCT; eukaryotic type II chaperonin complex; cyclin;
KW binding agent; substrate-binding site; SBS; substrate folding; actin;
KW tubulin; treatment; cancer; anticancer drug; viral infection; screening;
KW reduced toxicity.

XX OS Synthetic.

XX PN WO9853322-A1.

XX PD 26-NOV-1998.

XX PF 22-MAY-1998; 98WO-GB001485.

XX PR 23-MAY-1997; 97GB-00010762.

XX PA (CANC-) INST CANCER RES ROYAL CANCER HOSPITAL.

XX PI Willison K, Hynes G, Liou AK;

XX PT WPI, 1999-070162/06.

XX PT Identifying specific binding agents for substrate binding site in CCT
chaperonin complex - also new peptide binding agents and their mimetics,
cancer.

XX PS Disclosure; Fig 10; 97pp; English.

XX CC This invention describes a method which uses the CCT (eukaryotic type II
chaperonin) complex or part of it, for identifying a binding agent that
can occupy a substrate-binding site (SBS) on the CCT complex. By binding
to the CCT complex, the binding agents block an SBS so that biological
activity of the CCT complex is affected, particularly its ability to fold
substrates such as actin, tubulin and cyclin. The binding agents are
useful for treatment of cancer, particularly when used in combination
with an anticancer drug, or viral infections. Nucleic acid fragments are
used to screen for agents, e.g. binding agents that modulate interaction
between the CCT complex and a protein that is to be folded. The binding

Aag50873 Arabidops
Aag05583 Arabidops
Aag50944 Arabidops
Aag54243 Arabidops
Aag06484 Arabidops
Adi63011 Human apo
Aag06483 Arabidops
Aag05872 Arabidops
Aag05582 Arabidops
Aag54242 Arabidops
Aag50943 Arabidops
Aab12985 Human det
Aap61532 Sequence
Abb77395 Human act
Abr64271 Angiogene
Aam04830 Rat cytop
Adm85212 Rat actin
Ade61174 Rat Prote
Adf30525 Rat angio
Adi63062 Human apo

74 100.0 332 3 AAG50873
74 100.0 332 3 AAG05583
74 100.0 332 3 AAG50944
74 100.0 332 3 AAG54243
74 100.0 332 3 AAG06484
74 100.0 332 7 ADI63011
74 100.0 360 3 AAG06483
74 100.0 360 3 AAG50872
74 100.0 360 3 AAG05582
74 100.0 360 3 AAG54242
74 100.0 360 3 AAG50943
74 100.0 374 3 AAB12985
74 100.0 375 1 AAP61532
74 100.0 375 5 ABB77395
74 100.0 375 6 ABR64271
74 100.0 375 6 AAM04830
74 100.0 375 7 ADM85212
74 100.0 375 7 ADE61174
74 100.0 375 7 ADF30525
74 100.0 375 7 ADI63062

CC agents may target cells that are actively synthesising tubulin etc.
CC (unlike known microtubule-stabilising agents that affect all cells), so
CC should have reduced toxicity for normal cells. AA92527-W92541 are
CC peptide substrates used in the method of the invention

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. NO. 3.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPAMYVAIQAVL 15
Db 1 TFNTPAMYVAIQAVL 15
|||||

RESULT 2
AA13687
ID AA13687 standard; protein; 97 AA.

XX AC AA13687;

XX DT 12-OCT-2001 (first entry)

XX DE Peptide #121 encoded by probe for measuring cervical gene expression.

XX KW Probe; human; microarray; gene expression; cervical epithelial cell;
cervical cancer.

XX OS Homo sapiens.

XX PN WO200157278-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000670.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488901/53.

XX PS Claim 27; SEQ ID NO 18513; 487pp; English.

XX CC The present invention relates to human single exon nucleic acid probes
(SENPs: see A110068-AA128459). The present sequence is a peptide encoded
by one such probe. The SENPs are derived from human HeLa cells. The SENPs
can be used to produce a single exon microarray, which can be used for
measuring human gene expression in a sample derived from human cervical
epithelial cells. By measuring gene expression, the probes are therefore
useful in grading and/or staging of diseases of the cervix, notably
cervical cancer. Note: The sequence data for this patent did not form
part of the printed specification, but was obtained in electronic format
directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 97 AA;

Query Match 100.0%; Score 74; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. NO. 3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPAMYVAIQAVL 15
Db 5 TFNTPAMYVAIQAVL 19
|||||

RESULT 3
ABB32618

ID ABB32618 standard; peptide; 97 AA.

XX AC ABB32618;

XX DT 04-FEB-2002 (first entry)

XX DE Peptide #124 encoded by human foetal liver single exon probe.

XX KW Human; foetal liver; gene expression; single exon nucleic acid probe.

XX OS Homo sapiens.

XX PN WO200157277-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000669.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483447/52.

XX PS Claim 27; SEQ ID NO 25253; 639pp + Sequence Listing; English.

XX CC The invention relates to a single exon nucleic acid probe for measuring
human gene expression in a sample derived from human foetal liver. The
single exon nucleic acid probes may be used for predicting, measuring and
displaying gene expression in samples derived from human foetal liver. The
present sequence is a peptide encoded by a single exon nucleic acid probe
of the invention. Note: The sequence data for this patent did not form
part of the printed specification, but was obtained in electronic format
directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 97 AA;

Query Match 100.0%; Score 74; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. NO. 3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPAMYVAIQAVL 15
Db 5 TFNTPAMYVAIQAVL 19
|||||

RESULT 4
AA26087

ID AA26087 standard; protein; 97 AA.

XX AC AA26087;

XX DT 17-OCT-2001 (first entry)

XX DE Peptide #124 encoded by probe for measuring placental gene expression.

XX Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.

XX Homo sapiens.

XX WO200157272-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000663.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human placenta.

XX Claim 27; SEQ ID NO 26356; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENPs;
CC see AA131315-A157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders

XX Sequence 97 AA;

Query Match 100.0%; Score 74; DB 4; Length 97;

Best Local Similarity 100.0%; Pred. No. 3e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPMYVAIQAVL 15

Db 5 TFNTPMYVAIQAVL 19

RESULT 5

ABB27467

ID ABB27467 standard; peptide; 97 AA.

XX ABB27467;

XX 01-FEB-2002 (first entry)

XX Human peptide #118 encoded by breast cell single exon nucleic acid probe.

XX Human; microarray; single exon probe; gene expression; breast; disease;

XX cancer.

XX Homo sapiens.

XX WO200157271-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000662.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-496933/54.

XX New spatially-addressable set of single exon nucleic acid probes, useful

XX for measuring gene expression in sample derived from human breast,

XX comprises number of single exon nucleic acid probes.

XX Claim 27; SEQ ID NO 10435; 327pp + Sequence Listing; English.

XX The invention relates to a spatially-addressable set of single exon

XX nucleic acid probes for measuring gene expression in a sample derived

XX from human breast and BT 474 cells. The method involves contacting the

XX probes with a collection of detectably labelled nucleic acids derived

XX from mRNA of human breast, and then measuring the label bound to each

XX probe of the microarray. The probes are useful for verifying the

XX expression of regions of genomic DNA predicted to encode proteins. They

XX are useful for gene discovery, and for determining predisposition and/or

XX assessing the toxicity of chemical agents on cells. The microarray of

XX this invention presents a far greater diversity of probes for measuring

XX gene expression, with far less bias than expressed sequence tag

XX microarrays. The method is suitable for rapid production of functional

XX information from genomic sequence. The present sequence is a peptide

XX encoded by a single exon nucleic acid probe of the invention. Note: The

XX sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from WIPO

XX at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 97 AA;

Query Match 100.0%; Score 74; DB 4; Length 97;

Best Local Similarity 100.0%; Pred. No. 3e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPMYVAIQAVL 15

Db 5 TFNTPMYVAIQAVL 19

RESULT 6

ABB18116

ID ABB18116 standard; protein; 97 AA.

XX ABB18116;

XX 23-JAN-2002 (first entry)

XX Protein #115 encoded by probe for measuring heart cell gene expression.

XX Human; gene expression; heart; microarray; vascular system;

XX cardiovascular disease; hypertension; cardiac arrhythmia;

XX congenital heart disease.

XX Homo sapiens.

XX WO200157274-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000666.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.


```
Query Match      100.0%; Score 74; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPMYVAIQAVL 15
Db 5 TFNTPMYVAIQAVL 19
|||||

RESULT 9
ID ABG47471 standard; peptide; 97 AA.
XX AC ABG47471;
XX DT 25-FEB-2003 (first entry)
XX DE Human liver peptide, SEQ ID No 26119.
XX KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
XX KW hypercholesterolaemia; coronary heart disease.
XX OS Homo sapiens.
XX PN WO200157273-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000664.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488898/53.
XX DR Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human adult liver.
XX PS Claim 27; SEQ ID NO 26119; 658pp; English.
XX CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
XX CC measuring human gene expression in a sample derived from human adult
XX CC liver, comprising one of 13109 defined nucleotide sequences given in the
XX CC specification (or complements/ fragments). The probe hybridises at high
XX CC stringency to a nucleic acid molecule expressed in the human adult liver.
XX CC (I) may be used for predicting, measuring and displaying gene expression
XX CC in samples derived from human adult liver. The genes identified may be
XX CC involved in genetic liver diseases such as cirrhosis,
XX CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
XX CC associated with coronary heart disease. ABG47348-ABG59930 represent human
XX CC liver single exon encoded peptides of the invention. Note: The sequence
XX CC information for this patent does not appear in the printed specification
XX CC but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 97 AA;

Query Match      100.0%; Score 74; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPMYVAIQAVL 15
Db 5 TFNTPMYVAIQAVL 19
|||||

RESULT 11
ID ABG35459 standard; peptide; 97 AA.
XX AC ABG35459;
XX ABG35459;
```

```
Db 5 TFNTPMYVAIQAVL 19

RESULT 10
ID AAM01437 standard; protein; 97 AA.
XX AC AAM01437;
XX DT 09-OCT-2001 (first entry)
XX DE Peptide #119 encoded by probe for measuring human breast gene expression.
XX DE Probe; human; breast disease; breast cancer; development disorder;
XX KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX OS Homo sapiens.
XX PN WO200157270-A2.
XX PD 09-AUG-2001.
XX PF 29-JAN-2001; 2001WO-US000661.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-476286/51.
XX DR Novel single exon nucleic acid probe used to measuring gene expression in
XX PT a human breast.
XX PS Claim 27; SEQ ID NO 10177; 322pp; English.
XX CC The present invention relates to novel single exon nucleic acid probes
XX CC (see AAI00010-AAI10067). The present sequence is a peptide encoded by one
XX CC such probe. The probes are useful for measuring human gene expression in
XX CC a human breast sample, where the probe hybridises at high stringency to a
XX CC nucleic acid expressed in the human breast. The probes are useful for
XX CC predicting, diagnosing, grading, staging, monitoring and prognosing
XX CC diseases of the human breast, particularly those diseases with polygenic
XX CC aetiology. The diseases include: breast cancer, disorders of developmental
XX CC inflammatory diseases of the breast, fibrocystic changes, proliferative
XX CC breast disease and non-carcinoma tumours. Note: The sequence data for
XX CC this patent did not form part of the printed specification, but was
XX CC obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 97 AA;

Query Match      100.0%; Score 74; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPMYVAIQAVL 15
Db 5 TFNTPMYVAIQAVL 19
|||||

RESULT 11
ID ABG35459 standard; peptide; 97 AA.
XX AC ABG35459;
```

XX 19-AUG-2002 (first entry)
 XX Human peptide encoded by genome-derived single exon probe SEQ ID 25124.
 XX
 XX Human; single exon probe; asthma; lung cancer; COPD; ILD;
 XX chronic obstructive pulmonary disease; interstitial lung disease;
 XX familial idiopathic pulmonary fibrosis; neurofibromatosis;
 XX tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 XX Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 XX pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 XX pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 XX primary ciliary dyskinesia; pulmonary hypertension;
 XX hyaline membrane disease.
 XX
 XX Homo sapiens.
 XX
 XX WO200186003-A2.
 XX
 XX 15-NOV-2001.
 XX
 XX 30-JAN-2001; 2001WO-US000665.
 XX
 XX 04-FEB-2000; 2000US-0180312P.
 XX 26-MAY-2000; 2000US-0207456P.
 XX 30-JUN-2000; 2000US-00608408.
 XX 03-AUG-2000; 2000US-00632366.
 XX 21-SEP-2000; 2000US-0234687P.
 XX 27-SEP-2000; 2000US-0236359P.
 XX 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2002-114183/15.
 XX
 XX Spatially-addressable set of single exon nucleic acid probes, used to
 XX measure gene expression in human lung samples.
 XX
 XX Claim 27; SEQ ID NO 25124; 634pp; English.
 XX
 XX The invention relates to a spatially-addressable set of single exon
 XX nucleic acid probes for measuring gene expression in a sample derived
 XX from human lung comprising single exon nucleic acid probes having one of
 XX 12614 nucleic acid sequences mentioned in the specification, or their
 XX complements or the 12387 open reading frames derived from the 12614
 XX probes. Also included are a microarray comprising the novel set of probes
 XX; the novel set of probes which hybridise at high stringency to a nucleic
 XX acid expressed in the human lung; measuring gene expression in a sample
 XX derived from human lung, comprising (a) contacting the array with a
 XX collection of detectably labeled nucleic acids derived from human lung
 XX mRNA, and (b) measuring the label detectably bound to each probe of the
 XX array; identifying exons in a eukaryotic genome, comprising (a)
 XX algorithmically predicting at least one exon from genomic sequences of
 XX the eukaryote; and (b) detecting specific hybridisation of detectably
 XX labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 XX having a fragment identical to the predicted exon, the probe is included
 XX in the above mentioned microarray; assigning exons to a single gene,
 XX comprising (a) identifying exons from genomic sequence by the method
 XX above and (b) measuring the expression of each of the exons in several
 XX tissues and/or cell types using hybridisation to a single exon
 XX microarrays having a probe with the exon, where a common pattern of
 XX expression of the exons in the tissues and/or cell types indicates that
 XX the exons should be assigned to a single gene; a peptide comprising one
 XX of 12011 sequences, mentioned in the specification, or encoded by the
 XX probes/open reading frames (ORF). The probes are used for gene expression
 XX analysis; and for identifying exons in a gene, particularly using human
 XX lung derived mRNA and for the study of lung diseases such as asthma, lung
 XX cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 XX disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 XX tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 XX Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary

CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
 CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 CC present sequence is a peptide/protein encoded by a single exon probe of
 CC the invention. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 97 AA;
 XX
 XX Query Match 100.0%; Score 74; DB 5; Length 97;
 XX Best Local Similarity 100.0%; Pred. No. 3e-06;
 XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 T F T N P A M Y V A I Q A V L 15
 XX | | | | | | | | | | | | | | |
 XX Db 5 T F T N P A M Y V A I Q A V L 19
 XX
 XX RESULT 12
 XX AAU33076
 XX ID AAU33076 standard; protein; 137 AA.
 XX
 XX AC AAU33076;
 XX
 XX DT 18-DEC-2001 (first entry)
 XX
 XX DE Novel human secreted protein #3567.
 XX
 XX KW Human; vaccination; gene therapy; nutritional supplement;
 XX stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 XX KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 XX OS Homo sapiens.
 XX
 XX PN WO200179449-A2.
 XX
 XX PD 25-OCT-2001.
 XX
 XX PF 16-APR-2001; 2001WO-US008656.
 XX
 XX PR 18-APR-2000; 2000US-00552929.
 XX 26-JAN-2001; 2001US-00770160.
 XX
 XX PR (HYSE-) HYSEQ INC.
 XX
 XX PA Tang YT, Liu C, Drmanac RT;
 XX
 XX PI WPI; 2001-611725/70.
 XX
 XX DR Nucleic acids encoding a range of human polypeptides, useful in genetic
 XX vaccination, testing and therapy.
 XX
 XX PT Claim 20; Page 704-705; 765pp; English.
 XX
 XX The invention relates to novel human secreted polypeptides. The
 XX polypeptides and antibodies to the polypeptides are useful for
 XX determining the presence of or predisposition to a disease associated
 XX with altered levels of polypeptide. The polypeptides are also useful for
 XX identifying agents (agonists and antagonists) that bind to them. Cells
 XX expressing the proteins are useful for identifying a therapeutic agent
 XX for use in treatment of a pathology related to aberrant expression or
 XX physiological interactions of the polypeptide. Vectors comprising the
 XX nucleic acids encoding the polypeptides and cells genetically engineered
 XX to express them are also useful for producing the proteins. The proteins
 XX are useful in genetic vaccination, testing and therapy, and can be used
 XX as nutritional supplements. They may be used to increase stem cell
 XX proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
 XX and/or nerve tissue growth or regeneration; immune suppression and/or
 XX stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
 XX AAU29510-AAU33304 represent the amino acid sequences of novel human
 XX secreted proteins of the invention

SQ Sequence 137 AA;
Query Match 100.0%; Score 74; DB 4; Length 137;
Best Local Similarity 100.0%; Pred. No. 4.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPAMYVAIOAVL 15
| | | | | | | | | | | | | | | |
Db 70 TFNTPAMYVAIOAVL 84

RESULT 13
ABG15101
ID ABG15101 standard; protein; 150 AA.
XX
AC ABG15101;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #15092.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
FN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS79288.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 45460; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 150 AA;

Query Match 100.0%; Score 74; DB 4; Length 150;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPAMYVAIOAVL 15
| | | | | | | | | | | | | | | |
Db 88 TFNTPAMYVAIOAVL 102

RESULT 14
ABG26869
ID ABG26869 standard; protein; 166 AA.
XX
AC ABG26869;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #26860.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
FN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS91056.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 57228; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 166 AA;

Query Match 100.0%; Score 74; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTNTPAMYVAIQAVL 15
 DB 137 TTNTPAMYVAIQAVL 151

RESULT 15
 ABP42912
 ID ABP42912 standard; protein; 168 AA.
 XX
 AC ABP42912;
 XX
 DT 22-AUG-2002 (first entry)
 XX
 DE Human ovarian antigen HPDQ265, SEQ ID NO:4044.
 XX
 KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive.
 XX
 OS Homo sapiens.
 XX
 PN WO200200677-A1.
 XX
 PD 03-JAN-2002.
 XX
 PF 07-JUN-2001; 2001WO-US018569.
 XX
 PR 07-JUN-2000; 2000US-0209467P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Birse CE, Rosen CA;
 XX
 DR WPI; 2002-147878/19.
 DR N-PSDB; ABQ55989.
 XX
 PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 PT cancer), immune disorders, cardiovascular disorders and neurological
 PT diseases.
 XX
 PS Claim 11; SEQ ID NO 4044; 2922pp; English.
 XX
 CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovary and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia). Cardiovascular disorders
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may

further be used for gene therapy, chromosome mapping, in the
 identification of individuals and in forensic analysis, and the
 polypeptides may be used as food additives or to prepare antibodies
 useful in disease diagnosis, drug targeting and phenotyping. The present
 sequence represents a human ovarian antigen of the invention. Note: The
 sequence data for this patent did not form part of the printed
 specification, but was obtained in electronic format directly from WIPO
 at ftp.wipo.int/pub/published_pct_sequences

Sequence 168 AA;
 Query Match 100.0%; Score 74; DB 5; Length 168;
 Best Local Similarity 100.0%; Pred. No. 5.7e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTNTPAMYVAIQAVL 15
 DB 12 TTNTPAMYVAIQAVL 26

Search completed: April 8, 2005, 10:50:45
 Job time : 64.4 secs

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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:57 ; Search time 17.5333 Seconds
(without alignments)
63.863 Million cell updates/sec

Title: US-09-423-351C-6

Perfect score: 74

Sequence: 1 TFPNPMYVAIQAVL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.psp:*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.psp:*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.psp:*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.psp:*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.psp:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.psp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	374	3	US-08-609-236-6
2	74	100.0	375	4	US-09-976-594-731
3	74	100.0	399	4	US-09-949-016-9424
4	74	100.0	404	4	US-09-949-016-11313
5	69	93.2	375	3	US-09-106-217-16
6	69	93.2	376	1	US-08-588-113-2
7	69	93.2	376	4	US-09-949-016-6100
8	69	93.2	377	3	US-09-106-217-2
9	69	93.2	377	4	US-09-919-172-33
10	69	93.2	377	4	US-09-917-254-53
11	69	93.2	386	4	US-09-949-016-7721
12	69	93.2	402	4	US-09-949-016-10757
13	68	91.9	146	3	US-09-306-446C-5
14	68	91.9	374	3	US-09-306-446C-2
15	64	86.5	375	2	US-08-494-151-14
16	61	82.4	371	1	US-08-261-206A-77
17	61	82.4	375	3	US-09-171-337A-7
18	61	82.4	375	3	US-09-171-337A-8
19	61	82.4	375	4	US-09-631-022-7
20	61	82.4	375	4	US-09-631-022-8
21	61	82.4	477	4	US-09-248-796A-14109
22	56	75.7	445	4	US-09-949-016-8556
23	55	74.3	362	4	US-09-949-016-7725
24	55	74.3	376	4	US-09-538-092-1109
25	55	74.3	376	4	US-09-538-092-1110
26	55	74.3	376	4	US-09-949-016-6656
27	55	74.3	376	4	US-09-949-016-8452

28	51	68.9	336	4	US-09-248-796A-14108	Sequence 14108, A
29	47	63.5	365	4	US-09-248-796A-20619	Sequence 20619, A
30	42	56.8	394	4	US-09-949-016-6655	Sequence 6655, Ap
31	42	56.8	406	4	US-09-949-016-7396	Sequence 7396, Ap
32	40	54.1	620	3	US-09-232-200-49	Sequence 49, Appl
33	40	54.1	620	3	US-09-232-197-49	Sequence 49, Appl
34	40	54.1	620	3	US-09-232-201-49	Sequence 49, Appl
35	40	54.1	620	4	US-09-232-195-49	Sequence 49, Appl
36	40	54.1	687	4	US-09-949-016-10593	Sequence 10593, A
37	38	51.4	495	4	US-09-270-767-44726	Sequence 44726, A
38	38	51.4	620	3	US-09-232-200-61	Sequence 61, Appl
39	38	51.4	620	3	US-09-232-200-93	Sequence 93, Appl
40	38	51.4	620	3	US-09-232-197-61	Sequence 61, Appl
41	38	51.4	620	3	US-09-232-197-93	Sequence 93, Appl
42	38	51.4	620	3	US-09-232-201-61	Sequence 61, Appl
43	38	51.4	620	3	US-09-232-201-93	Sequence 93, Appl
44	38	51.4	620	4	US-09-232-195-61	Sequence 61, Appl
45	38	51.4	620	4	US-09-232-195-93	Sequence 93, Appl

ALIGNMENTS

RESULT 1
US-08-609-236-6
; Sequence 6, Application US/08609236
; Patent No. 6087398
; GENERAL INFORMATION:
; APPLICANT: Steven R. Goodman
; TITLE OF INVENTION: NO. 6087398e1 Sickle Cell Anemia Treatment
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McGregor & Adler, LLP
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,236
; FILING DATE: March 1, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/002,288
; FILING DATE: August 14, 1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Benjamin Aaron Adler, Ph.D.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5807
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6908
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374
; TYPE: Amino acid
; STRANDEDNESS:
; TOPOLOGY: Linear
; MOLECULE TYPE:
; DESCRIPTION: Protein
; HYPOTHETICAL: No
; ANTI-SENSE: No
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:

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; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; US-08-609-236-6

Query Match      100.0%; Score 74; DB 3; Length 374;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TFTPAMYVAIQAVL 15
DB      125 TFTPAMYVAIQAVL 139

RESULT 2
US-09-976-594-731
; Sequence 731, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 731
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1837317CD1
US-09-976-594-731

Query Match      100.0%; Score 74; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TFTPAMYVAIQAVL 15
DB      126 TFTPAMYVAIQAVL 140

RESULT 3
US-09-949-016-9424
; Sequence 9424, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9424
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9424

Query Match      100.0%; Score 74; DB 4; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TFTPAMYVAIQAVL 15
DB      155 TFTPAMYVAIQAVL 169

RESULT 4
US-09-949-016-11313
; Sequence 11313, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11313
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11313

Query Match      100.0%; Score 74; DB 4; Length 404;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TFTPAMYVAIQAVL 15
DB      155 TFTPAMYVAIQAVL 169

RESULT 5
US-09-106-217-16
; Sequence 16, Application US/09106217
; Patent No. 6063576
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Olson, Timothy M.
; TITLE OF INVENTION: Actin Mutations in Dilated
; TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,217
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 2323-125
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; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; US-08-609-236-6

Query Match      100.0%; Score 74; DB 3; Length 374;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TFTPAMYVAIQAVL 15
DB      125 TFTPAMYVAIQAVL 139

RESULT 2
US-09-976-594-731
; Sequence 731, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 731
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1837317CD1
US-09-976-594-731

Query Match      100.0%; Score 74; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TFTPAMYVAIQAVL 15
DB      126 TFTPAMYVAIQAVL 140

RESULT 3
US-09-949-016-9424
; Sequence 9424, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9424
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9424

Query Match      100.0%; Score 74; DB 4; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TFTPAMYVAIQAVL 15
DB      155 TFTPAMYVAIQAVL 169

RESULT 4
US-09-949-016-11313
; Sequence 11313, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9424
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9424

Query Match      100.0%; Score 74; DB 4; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TFTPAMYVAIQAVL 15
DB      155 TFTPAMYVAIQAVL 169

RESULT 5
US-09-106-217-16
; Sequence 16, Application US/09106217
; Patent No. 6063576
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Olson, Timothy M.
; TITLE OF INVENTION: Actin Mutations in Dilated
; TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,217
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 2323-125
```

TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-106-217-16

Query Match 93.2%; Score 69; DB 3; Length 375;
Best Local Similarity 93.3%; Pred. No. 0.00011;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTNTPAMYVAIQAVL 15
Db 126 TTNVPMYVAIQAVL 140
||| |||||

RESULT 6

US-08-588-113-2
; Sequence 2, Application US/08588113

Patent No. 5710003
; GENERAL INFORMATION:

APPLICANT: McHugh, Kirk M.
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR DETERMINING
; TITLE OF INVENTION: MALIGNANCY OF SMOOTH MUSCLE TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5710003ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA

COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/588,113
; FILING DATE:

CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:
; NAME: Ralph, Rebecca L.
; REGISTRATION NUMBER: 35,152
; REFERENCE/DOCKET NUMBER: TJU-1652
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 376 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-588-113-2

Query Match 93.2%; Score 69; DB 1; Length 376;
Best Local Similarity 93.3%; Pred. No. 0.00011;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTNTPAMYVAIQAVL 15
Db 127 TTNVPMYVAIQAVL 141
||| |||||

RESULT 7

US-09-949-016-6100
; Sequence 6100, Application US/09949016

Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6100
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6100

Query Match 93.2%; Score 69; DB 4; Length 376;
Best Local Similarity 93.3%; Pred. No. 0.00011;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTNTPAMYVAIQAVL 15
Db 127 TTNVPMYVAIQAVL 141
||| |||||

RESULT 8

US-09-106-217-2
; Sequence 2, Application US/09106217

Patent No. 6063576
; GENERAL INFORMATION:

APPLICANT: Keating, Mark T.
; APPLICANT: Olson, Timothy M.
; TITLE OF INVENTION: Actin Mutations in Dilated
; TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; STREET: Tower
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,217
; FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 2323-125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-106-217-2

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Query Match      93.2%; Score 69; DB 3; Length 377;
Best Local Similarity 93.3%; Pred. No. 0.00011;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TTNTPAMYVAIQAVL 15
Db      128 TTNVPAMYVAIQAVL 142

RESULT 9
US-09-919-172-33
; Sequence 33, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 33
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 1709118CD1
US-09-919-172-33

Query Match      93.2%; Score 69; DB 4; Length 377;
Best Local Similarity 93.3%; Pred. No. 0.00011;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TTNTPAMYVAIQAVL 15
Db      128 TTNVPAMYVAIQAVL 142

RESULT 10
US-09-917-254-53
; Sequence 53, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
; APPLICANT: Mutter, George
; TITLE OF INVENTION: Prognostic Classification of Breast Cancer
; FILE REFERENCE: B0801/7224(JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/222,093
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 53
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-917-254-53

Query Match      93.2%; Score 69; DB 4; Length 377;
Best Local Similarity 93.3%; Pred. No. 0.00011;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TTNTPAMYVAIQAVL 15
Db      128 TTNVPAMYVAIQAVL 142

RESULT 11
US-09-919-172-33
; Sequence 33, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 33
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 1709118CD1
US-09-919-172-33

Query Match      93.2%; Score 69; DB 3; Length 377;
Best Local Similarity 93.3%; Pred. No. 0.00011;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TTNTPAMYVAIQAVL 15
Db      128 TTNVPAMYVAIQAVL 142

RESULT 12
US-09-949-016-10757
; Sequence 10757, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10757
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10757

Query Match      93.2%; Score 69; DB 4; Length 402;
Best Local Similarity 93.3%; Pred. No. 0.00012;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TTNTPAMYVAIQAVL 15
Db      153 TTNVPAMYVAIQAVL 167

RESULT 13
US-09-306-446C-5
; Sequence 5, Application US/09306446C
; Patent No. 6372959
; GENERAL INFORMATION:
; APPLICANT: KIM, Dong Soo
```

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; APPLICANT: KIM, Chul Geun
; APPLICANT: NAM, Yoon Kwon
; APPLICANT: NOH, Jae Koo
; APPLICANT: CHO, Kyoo Nam
; TITLE OF INVENTION: EXPRESSION VECTOR OF MUD LOACH GROWTH HORMONE GENE
; FILE REFERENCE: P06344USO/BAS
; CURRENT APPLICATION NUMBER: US/09/306.446C
; CURRENT FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: KR 98/20255
; PRIOR FILING DATE: 1998-06-01
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Misgurnus mizolepus
US-09-306-446C-5

Query Match 91.9%; Score 68; DB 3; Length 146;
Best Local Similarity 93.3%; Pred. No. 5.6e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 TFNTPAMYVAIQAVL 15
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Db 5 TFNTPAMYVAIQAVL 19

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RESULT 14
US-09-306-446C-2
; Sequence 2, Application US/09306446C
; Patent No. 6372959
; GENERAL INFORMATION:
; APPLICANT: KIM, Dong Soo
; APPLICANT: KIM, Chul Geun
; APPLICANT: NAM, Yoon Kwon
; APPLICANT: NOH, Jae Koo
; APPLICANT: CHO, Kyoo Nam
; TITLE OF INVENTION: EXPRESSION VECTOR OF MUD LOACH GROWTH HORMONE GENE
; FILE REFERENCE: P06344USO/BAS
; CURRENT APPLICATION NUMBER: US/09/306.446C
; CURRENT FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: KR 98/20255
; PRIOR FILING DATE: 1998-06-01
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Misgurnus mizolepus
US-09-306-446C-2

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Query Match 91.9%; Score 68; DB 3; Length 374;
Best Local Similarity 93.3%; Pred. No. 0.00017;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 TFNTPAMYVAIQAVL 15
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Db 126 TFNTPAMYVAIQAVL 140

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RESULT 15
US-08-494-151-14
; Sequence 14, Application US/08494151
; Patent No. 5840528
; GENERAL INFORMATION:
; APPLICANT: Van Ooyen, Albert Johannes Joseph
; TITLE OF INVENTION: Transformation of Phaffia rhodozyma
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESS: Morrison & Foerster
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington, D.C.
; COUNTRY: USA

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; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/494.151
; FILING DATE: 23-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20039.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-494-151-14

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Query Match 86.5%; Score 64; DB 2; Length 375;
Best Local Similarity 86.7%; Pred. No. 0.00092;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 TFNTPAMYVAIQAVL 15
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Db 126 TFNAPAFYVAIQAVL 140

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

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(without alignments)
116.718 Million cell updates/sec

Title: US-09-423-351C-6

Perfect score: 74

Sequence: 1 TFNTPAMTVAIQAVL 15

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- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	74	100.0	97	US-09-864-761-33414	Sequence 33414, A
2	74	100.0	168	US-10-264-049-4044	Sequence 4044, Ap
3	74	100.0	180	US-10-437-963-169247	Sequence 169247, Ap
4	74	100.0	197	US-10-424-599-280810	Sequence 280810, Ap
5	74	100.0	204	US-10-264-049-4148	Sequence 4148, Ap
6	74	100.0	208	US-10-424-599-282905	Sequence 282905, Ap
7	74	100.0	219	US-10-002-631C-56	Sequence 56, Appl
8	74	100.0	237	US-10-424-599-143226	Sequence 143226, Ap
9	74	100.0	261	US-10-424-599-177530	Sequence 177530, Ap
10	74	100.0	276	US-10-425-114-52089	Sequence 52089, A
11	74	100.0	299	US-10-424-599-278431	Sequence 278431, Ap
12	74	100.0	371	US-10-322-281-68	Sequence 68, Appl
13	74	100.0	375	US-10-205-194-93	Sequence 93, Appl

Sequence 88, Appl
Sequence 94, Appl
Sequence 82, Appl
Sequence 223492,
Sequence 278432,
Sequence 187415,
Sequence 280814,
Sequence 63, Appl
Sequence 1436, Ap
Sequence 3432, Ap
Sequence 42317, A
Sequence 37942, A
Sequence 162684, A
Sequence 44494, A
Sequence 69353, A
Sequence 57500, A
Sequence 59172, A
Sequence 58333,
Sequence 101, App
Sequence 33, Appl
Sequence 52, Appl
Sequence 64, Appl
Sequence 162009,
Sequence 162685,
Sequence 162686,
Sequence 283336,
Sequence 4, Appl
Sequence 148877,
Sequence 198295, A
Sequence 47239, A
Sequence 52458, A
Sequence 59265, A

ALIGNMENTS

RESULT 1

US-09-864-761-33414
; Sequence 33414, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30

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, PRIOR APPLICATION NUMBER: PCT/US01/006663
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/006662
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/006661
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/006670
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: US 60/234,687
, PRIOR FILING DATE: 2000-09-21
, PRIOR APPLICATION NUMBER: US 09/608,408
, PRIOR FILING DATE: 2000-06-30
, PRIOR APPLICATION NUMBER: US 09/774,203
, PRIOR FILING DATE: 2001-01-29
, NUMBER OF SEQ ID NOS: 49117
, SOFTWARE: Annonax Sequence Listing Engine
, SEQ ID NO 33414

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Query Match      100.0%; Score 74; DB 9; Length 97;
Best Local Similarity 100.0%; Pred. No. 9.4e-06;
Matches 15: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
US-10-264-049-4044
/ Sequence 4044, Application US/10264049
/ Publication No. US20040005579A1
/ GENERAL INFORMATION:
/ APPLICANT: Birse et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
/ FILE REFERENCE: PA133PI
/ CURRENT APPLICATION NUMBER: US/10/264,049
/ CURRENT FILING DATE: 2002-10-04
/ PRIOR APPLICATION NUMBER: PCT/US01/18569
/ PRIOR FILING DATE: 2001-06-07
/ PRIOR APPLICATION NUMBER: US 60/209,467
/ PRIOR FILING DATE: 2000-06-07
/ NUMBER OF SEQ ID NOS: 4360
/ SOFTWARE: PatentIn ver. 3.1
/ SEQ ID NO 4044
/ LENGTH: 168
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-264-049-4044

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Db 12 T F T P A M Y V A I Q A V L 26

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RESULT 3
US-10-437-963-169247
; Sequence 169247, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 169247
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_67695C.1.pep
US-10-437-963-169247

```

RESULT 4
US-10-424-599-280810
; Sequence 280810, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 280810
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(197)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_95594C.1.pgp
; US-10-424-599-280810

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Query Match      100.0%; Score 74; DB 15; Length 197;
Best Local Similarity 100.0%; Pred. NO. 2.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  TTNTPMYVAIQAVL 15
      |||||

```

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Db      128  TFTPAMYVAIQAVL 142
; Publication No. US20030157486A1
; GENERAL INFORMATION:
; APPLICANT: Graff, Jonathon M.
; APPLICANT: Muenster, Matthew
; TITLE OF INVENTION: METHODS TO IDENTIFY SIGNAL SEQUENCES
; FILE REFERENCE: A34943 090495.0243
; CURRENT APPLICATION NUMBER: US/10/002.631C
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/300,309
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-631C-56

Query Match      100.0%; Score 74; DB 14; Length 219;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TFTPAMYVAIQAVL 15
      |||||||
DB      153  TFTPAMYVAIQAVL 167

RESULT 8
US-10-424-599-143226
; Sequence 143226, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 143226
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(237)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_100347C.1.pep
US-10-424-599-143226

Query Match      100.0%; Score 74; DB 15; Length 237;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TFTPAMYVAIQAVL 15
      |||||||
DB      10  TFTPAMYVAIQAVL 24

RESULT 9
US-10-424-599-177530
; Sequence 177530, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
```

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Db      128  TFTPAMYVAIQAVL 142
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4148
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-4148

Query Match      100.0%; Score 74; DB 15; Length 204;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TFTPAMYVAIQAVL 15
      |||||||
DB      146  TFTPAMYVAIQAVL 160

RESULT 6
US-10-424-599-282905
; Sequence 282905, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 282905
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(208)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_97486C.1.pep
US-10-424-599-282905

Query Match      100.0%; Score 74; DB 15; Length 208;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TFTPAMYVAIQAVL 15
      |||||||
DB      128  TFTPAMYVAIQAVL 142

RESULT 7
US-10-002-631C-56
; Sequence 56, Application US/10002631C
```

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 177530
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_131325C.1.pep
US-10-424-599-177530

Query Match 100.0%; Score 74; DB 15; Length 261;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPAMYVAIQAVL 15
| | | | | | | | | | | | | | | | | | | | | |
Db 12 TFNTPAMYVAIQAVL 26

RESULT 10

US-10-425-114-52089
; Sequence 52089, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 52089
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Glycine max

; FEATURE:
; OTHER INFORMATION: Clone ID: 701149157_FLIJ.pep
US-10-425-114-52089

Query Match 100.0%; Score 74; DB 15; Length 276;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPAMYVAIQAVL 15
| | | | | | | | | | | | | | | | | | | | | |
Db 27 TFNTPAMYVAIQAVL 41

RESULT 11

US-10-424-599-278431
; Sequence 278431, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 278431
; LENGTH: 299

; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_93446C.1.pep
US-10-424-599-278431

Query Match 100.0%; Score 74; DB 15; Length 299;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPAMYVAIQAVL 15
| | | | | | | | | | | | | | | | | | | | | |
Db 50 TFNTPAMYVAIQAVL 64

RESULT 12

US-10-322-281-68
; Sequence 68, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-281-68

Query Match 100.0%; Score 74; DB 16; Length 371;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TENTPAMYVAIQAVL 15
| | | | | | | | | | | | | | | | | | | | | |
Db 126 TENTPAMYVAIQAVL 140

RESULT 13

US-10-205-194-93
; Sequence 93, Application US/10205194
; Publication No. US20030134301A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pincock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018201
; CURRENT APPLICATION NUMBER: US/10/205,194
; CURRENT FILING DATE: 5200-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Rattus rattus
; FEATURE:
; OTHER INFORMATION: Cytoplasmic gamma isoform of actin
US-10-205-194-93

Query Match 100.0%; Score 74; DB 14; Length 375;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: April 8, 2005, 12:50:59
Job time : 42.6667 secs

Qy 1 TFTPAMYVAIQAVL 15
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Db 126 TFTPAMYVAIQAVL 140

RESULT 14
US-10-316-253-88
; Sequence 88, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-88

Query Match 100.0%; Score 74; DB 14; Length 375;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFTPAMYVAIQAVL 15
|||||
Db 126 TFTPAMYVAIQAVL 140

RESULT 15
US-10-205-331-94
; Sequence 94, Application US/10205331
; Publication No. US20040058326A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pinnoch, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018199
; CURRENT APPLICATION NUMBER: US/10/205,331
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 94
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Cytoplasmic beta-actin
US-10-205-331-94

Query Match 100.0%; Score 74; DB 15; Length 375;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFTPAMYVAIQAVL 15
|||||
Db 126 TFTPAMYVAIQAVL 140

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 9.33333 Seconds
(without alignments)
154.634 Million cell updates/sec

Title: US-09-423-351C-6

Perfect score: 74

Sequence: 1 TFNTPAMYVAIQAVL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	195	2	actin beta - pig (
2	74	100.0	195	2	actin 85c - potato
3	74	100.0	308	2	actin 3 - fruit fl
4	74	100.0	327	2	actin (clone 302)
5	74	100.0	328	2	actin beta - grass
6	74	100.0	362	2	actin type 5, cyto
7	74	100.0	374	1	actin beta - bovin
8	74	100.0	374	1	actin gamma - bovi
9	74	100.0	374	2	gamma-actin - huma
10	74	100.0	375	1	actin beta - rat
11	74	100.0	375	1	actin beta, cytoek
12	74	100.0	375	1	actin - Acanthance
13	74	100.0	375	1	actin beta - chick
14	74	100.0	375	1	actin - slime mold
15	74	100.0	375	1	actin beta - human
16	74	100.0	375	1	actin gamma 1 - hu
17	74	100.0	375	1	actin beta - mouse
18	74	100.0	375	1	actin gamma - mous
19	74	100.0	375	1	actin beta, non-mu
20	74	100.0	375	1	actin gamma, cytos
21	74	100.0	375	2	actin beta-2, cyto
22	74	100.0	375	2	actin beta-1, cyto
23	74	100.0	375	2	actin beta, cytoeo
24	74	100.0	375	2	actin beta - goose
25	74	100.0	376	1	actin gamma, cytos
26	74	100.0	376	1	actin - slime mold
27	74	100.0	376	2	Actin-1A - nematod
28	74	100.0	376	2	actin, cytosolic -
29	74	100.0	376	2	actin 3-sub1 - bli

actin 15 - slime m
actin 4 - Caenotha
actin 1 and
actin 2 - Caenotha
hypothetical prote
actin - California
actin (clone 403)
actin 5 - Atlantic
actin 11 - Atlanti
actin 3 - Atlantic
actin beta, cytoek
actin A4 - silkwor
actin A3, cytosoli
actin 1 - rice
actin - common tob
actin 97 - potato

ALIGNMENTS

RESULT 1

S39777

actin beta - pig (fragments)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004

C:Accession: S39777

R:Adamski, J.; Husein, B.; Thole, H.H.; Groeschel-Stewart, U.; Jungblut, P.W.

Biochem. J. 296, 797-802, 1993

A>Title: Linkage of 17-beta-oestradiol dehydrogenase to actin by epsilon- (gamma-glutamyl

A:Reference number: S39777; MUID:94107247; PMID:8280079

A:Accession: S39777

A:Molecule type: Protein

A:Residues: 1-20;21-52;53-79;80-85;86-95;96-116;117-151;152-159;160-195 <ADA>

A:Cross-references: UNIPROT:Q7M3B0

C:Superfamily: actin

Query Match 100.0%; Score 74; DB 2; Length 195;

Best Local Similarity 100.0%; Pred. No. 5.2e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPAMYVAIQAVL 15

Db 60 TFNTPAMYVAIQAVL 74

RESULT 2

S20097

actin 85c - potato (fragment)

C:Species: Solanum tuberosum (potato)

C>Date: 22-Nov-1993 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004

C:Accession: S20097

R:Drouin, G.; Dover, G.A.

J. Mol. Evol. 31, 132-150, 1990

A>Title: Independent gene evolution in the potato actin gene family demonstrated by phyl

A:Reference number: S20092; MUID:91012599; PMID:2120451

A:Accession: S20097

A:Molecule type: DNA

A:Residues: 1-195 <DRO>

A:Cross-references: UNIPROT:P30170; EMBL:X55747; NID:g21541; PIDN:CAA39277.1; PID:g13455

C:Genetics:

A:Introns: 132/1

C:Superfamily: actin

C:Keywords: cytoskeleton; structural protein

Query Match 100.0%; Score 74; DB 2; Length 195;

Best Local Similarity 100.0%; Pred. No. 5.2e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPAMYVAIQAVL 15

Db 108 TFNTPAMYVAIQAVL 122

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RESULT 3
A03000
actin 3 - fruit fly (Drosophila melanogaster) (fragments)
C:Species: Drosophila melanogaster
C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: A03000
R:Fyrberg, E.A.; Bond, B.J.; Hershey, N.D.; Mixter, K.S.; Davidson, N.
Cell 24, 107-116, 1981
A:Title: The actin genes of Drosophila: protein coding regions are highly conserved but
A:Reference number: A03000; MUID:81210174; PMID:6263481
A:Accession: A03000
A:Molecule type: DNA
A:Residues: 1-308 <FYR>
A:Cross-references: UNIPROT:P02572
A:Note: there are 68 unsequenced residues between positions 160 and 161. Partial sequence
A:Note: the authors translated the codon GTT for residue 263 as Ile
C:Genetics:
A:Gene: FlyBase:Act42A
A:Cross-references: FlyBase:FBgn0000043
A:Map position: 42A
C:Superfamily: actin
C:Keywords: methylated amino acid
F:74/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 74; DB 2; Length 308;
Best Local Similarity 100.0%; Pred. No. 8.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPAMYVAIQAVL 15
| | | | | | | | | | | | | | |
Db 127 TFNTPAMYVAIQAVL 141

RESULT 4
S11452
actin (clone 302) - brine shrimp (fragment)
C:Species: Artemia sp. (brine shrimp)
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: S11452
R:Macias, M.T.; Sastre, L.
Nucleic Acids Res. 18, 5219-5225, 1990
A:Title: Molecular cloning and expression of four actin isoforms during Artemia developm
A:Reference number: S11450; MUID:90384823; PMID:2402445
A:Accession: S11452
A:Molecule type: mRNA
A:Residues: 1-327 <MAC>
A:Cross-references: UNIPROT:P18602; EMBL:X52604; NID:G5666; PIDN:CAA36837.1; PID:g829162
C:Superfamily: actin
C:Keywords: methylated amino acid; structural protein
F:25/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 74; DB 2; Length 327;
Best Local Similarity 100.0%; Pred. No. 9.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPAMYVAIQAVL 15
| | | | | | | | | | | | | | |
Db 78 TFNTPAMYVAIQAVL 92

RESULT 5
S05430
actin beta - grass carp
C:Species: Ctenopharyngodon idella (grass carp)
C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C:Accession: S05430
R:Liu, Z.; Zhu, Z.; Roberg, K.; Faras, A.J.; Guisee, K.S.; Kapuscinski, A.R.; Hackett, P.
Nucleic Acids Res. 17, 5850, 1989
A:Title: The beta-actin gene of carp (Ctenopharyngodon idella).
A:Reference number: S05430; MUID:89345185; PMID:2762162
A:Accession: S05430
A>Status: translation not shown
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```
A:Molecule type: DNA
A:Residues: 1-328 <LIU>
A:Cross-references: UNIPROT:P83751; EMBL:M25013
C:Genetics:
A:Introns: 41/3; 121/3; 268/1
C:Superfamily: actin
C:Keywords: cytoskeleton; methylated amino acid
F:73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 74; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 9.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TENTPAMYVAIQAVL 15
| | | | | | | | | | | | | | |
Db 126 TFNTPAMYVAIQAVL 140

RESULT 6
A26559
actin type 5, cytosolic - chicken
C:Species: Gallus gallus (chicken)
C>Date: 09-Sep-1987 #sequence_revision 09-Sep-1987 #text_change 05-Dec-1997
C:Accession: A26559
R:Bergsma, D.J.; Chang, K.S.; Schwartz, R.J.
Mol. Cell. Biol. 5, 1151-1162, 1985
A:Reference number: A26559; MUID:85213487; PMID:4000121
A:Accession: A26559
A:Molecule type: DNA
A:Residues: 1-362 <BER>
C:Superfamily: actin
C:Keywords: cytosol; methylated amino acid
F:74/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 74; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TENTPAMYVAIQAVL 15
| | | | | | | | | | | | | | |
Db 127 TFNTPAMYVAIQAVL 141

RESULT 7
ATB08
actin beta - bovine (tentative sequence)
C:Species: Bos primigenius taurus (cattle)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: E14185; A39105; A02999; A14185
R:VanDeckerckhove, J.; Weber, K.
Eur. J. Biochem. 90, 451-462, 1978
A:Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain
A:Reference number: A14185; MUID:79045349; PMID:213279
A:Accession: E14185
A:Molecule type: protein
A:Residues: 1-374 <VAN>
A:Cross-references: UNIPROT:P60712
A:Note: only peptides that differed in composition from the corresponding peptides of rai
R:Degen, J.L.; Neubauer, M.G.; Degen, S.U.F.; Seyfried, C.E.; Morris, D.R.
J. Biol. Chem. 258, 12153-12162, 1983
A:Title: Regulation of protein synthesis in mitogen-activated bovine lymphocytes. Analys
A:Reference number: A39105; MUID:84032385; PMID:6195151
A:Accession: A39105
A:Molecule type: mRNA
A:Residues: 76-227;344-374 <DEG>
A:Cross-references: GB:K00622; GB:K00623
A:Note: actins beta and gamma were not distinguished in this study
C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
C:Superfamily: actin
C:Keywords: blocked amino end; cell motility; cytoskeleton; methylated amino acid; micro
F:17/Modified site: blocked amino end (Asp) (probably acetylated) #status experimental
F:72/Modified site: 3'-methylhistidine (His) #status predicted
```


Query Match 100.0%; Score 74; DB 1; Length 374;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPAMYVAIQAVL 15
 |||||
 Db 125 TFNTPAMYVAIQAVL 139

RESULT 8
 ATBOG
 actin gamma - bovine (tentative sequence)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
 C:Accession: B14185; A02999
 R:Vanderkerckhove, J.; Weber, K.
 Eur. J. Biochem. 90, 451-462, 1978
 A:Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain
 A:Reference number: A14185; MUID:79045349; PMID:213279
 A:Accession: B14185
 A:Molecule type: protein
 A:Residues: 1-374 <VAN>
 A:Cross-references: UNIPROT:P02571
 A:Note: Only peptides that differed in composition from the corresponding peptides of rat
 C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
 C:Superfamily: actin
 C:Keywords: blocked amino end; cell motility; cytoskeleton; methylated amino acid; micro
 F:1/Modified site: blocked amino end (Glu) (probably acetylated) #status experimental
 F:72/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 74; DB 1; Length 374;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPAMYVAIQAVL 15
 |||||
 Db 125 TFNTPAMYVAIQAVL 139

RESULT 9
 JC5818
 gamma-actin - human
 C:Species: Homo sapiens (man)
 C:Date: 20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
 C:Accession: JC5818; PC4501
 R:Hauschildt, S.; Schwarz, C.; Heine, H.; Ulmer, A.J.; Flad, H.D.; Rietschel, E.T.; Jene
 Biochem. Biophys. Res. Commun. 241, 670-674, 1997
 A:Title: Actin: A target of lipopolysaccharid-induced phosphorylation in human monocytes
 A:Reference number: JC5818; MUID:98096379; PMID:9434766
 A:Accession: JC5818
 A:Molecule type: protein
 A:Residues: 1-374 <HAU>
 A:Cross-references: UNIPROT:P02571
 A:Experimental source: monocyte
 A:Molecule type: protein
 A:Residues: 1-61;84-112;147-190;196-209;215-253;335-358 <HA2>
 A:Experimental source: monocyte
 C:Comment: This protein is involved in a signal transduction that eventually leads to mo
 C:Superfamily: actin

Query Match 100.0%; Score 74; DB 2; Length 374;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPAMYVAIQAVL 15
 |||||
 Db 125 TFNTPAMYVAIQAVL 139

RESULT 10
 ATRTC
 actin beta - rat

C:Species: Rattus norvegicus (Norway rat)
 C:Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 22-Jun-1999
 C:Accession: A38571; A02999
 R:Nudel, U.; Zakut, R.; Shani, M.; Neuman, S.; Levy, Z.; Yaffe, D.
 Nucleic Acids Res. 11, 1759-1771, 1983
 A:Title: The nucleotide sequence of the rat cytoplasmic beta-actin gene.
 A:Reference number: A38571; MUID:83168920; PMID:6300777
 A:Accession: A38571
 A:Molecule type: DNA
 A:Residues: 1-375 <NUD>
 A:Cross-references: GB:J00691; NID:G202653; PIDN:AAA40657.1; PID:G202654
 C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
 C:Genetics:
 A:Introns: 41/3; 121/3; 268/1; 328/3
 C:Superfamily: actin
 C:Keywords: cell motility; cytoskeleton; methylated amino acid; microfilament; mitosis;
 F:2-375/Product: actin beta #status predicted <MAT>
 F:73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 74; DB 1; Length 375;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPAMYVAIQAVL 15
 |||||
 Db 126 TFNTPAMYVAIQAVL 140

RESULT 11
 A48324
 actin beta, cytoskeletal - common carp
 C:Species: Cyprinus carpio (common carp)
 C:Date: 03-Feb-1994 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
 C:Accession: A48324
 R:Liu, Z.; Zhu, Z.; Roberg, K.; Faras, A.; Guise, K.; Kapuscinski, A.R.; Hackett, P.B.
 DNA Seq. 1, 125-136, 1990
 A:Title: Isolation and characterization of beta-actin gene of carp (Cyprinus carpio).
 A:Reference number: A48324; MUID:92190540; PMID:2134183
 A:Accession: A48324
 A:Molecule type: DNA
 A:Residues: 1-375 <LIU>
 A:Cross-references: UNIPROT:P83750; GB:M24113; NID:G213041; PIDN:AAA6886.1; PID:G213042
 A:Note: the authors translated the codon TTC for residue 21 as Pro, AAG for residue 50 a
 7 as Pro
 A:Note: the authors failed to translated the codon GGT for residue 42 as Gly
 C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
 C:Genetics:
 A:Introns: 41/3; 121/3; 268/3; 328/3
 C:Superfamily: actin
 C:Keywords: acetylated amino end; cell motility; cytoskeleton; methylated amino acid; mi
 F:2-375/Product: actin beta, cytoskeletal #status predicted <MAT>
 F:2/Modified site: acetylated amino end (Asp) (in mature form) #status predicted
 F:73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 74; DB 1; Length 375;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPAMYVAIQAVL 15
 |||||
 Db 126 TFNTPAMYVAIQAVL 140

RESULT 12
 ATAX
 actin - Acanthamoeba castellanii
 C:Species: Acanthamoeba castellanii
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
 C:Accession: A92886; A03004
 R:Nellen, W.; Gallwitz, D.
 J. Mol. Biol. 159, 1-18, 1982
 A:Title: Actin genes and actin messenger RNA in Acanthamoeba castellanii. Nucleotide se
 A:Reference number: A92886; MUID:83033627; PMID:6290670

A;Accession: A92886
A;Molecule type: DNA
A;Residues: 1-375 <NLE>
A;Cross-references: UNIPROT:P02578; GB:V00002; GB:J01016; NID:G5565; PIDN:CAA23399.1; PI
C;Comment: There are at least three actin genes in A. castellanii.
C;Genetics:
A;Introns: 105/3
C;Superfamily: actin
C;Keywords: methylated amino acid
F;73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 74; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTPTAMYVAIQAVL 15
|||||
Db 126 TTTPTAMYVAIQAVL 140

RESULT 13
ATHUB
actin beta - chicken
C;Species: Gallus gallus (chicken)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C;Accession: A20888; I50154
R;Kost, T.A.; Theodorakis, N.; Hughes, S.H.
Nucleic Acids Res. 11, 8287-8301, 1983
A;Title: The nucleotide sequence of the chick cytoplasmic beta-actin gene.
A;Reference number: A20888; MUID:84169478; PMID:6324080
A;Accession: A20888
A;Molecule type: DNA
A;Residues: 1-375 <KOS>
A;Cross-references: UNIPROT:P60706; EMBL:X00182
A;Note: the sequence shown follows the authors' translation at position 336
R;Chang, K.
Mol. Cell. Biol. 4, 2498-2508, 1984
A;Title: Isolation and characterization of six different chicken actin genes.
A;Reference number: I50153; MUID:85085956; PMID:6513927
A;Accession: I50154
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-17 <CHA>
A;Cross-references: GB:K02259; NID:g211086; PIDN:AAA49572.1; PID:g211087
C;Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
C;Genetics:
A;Introns: 41/3; 121/3; 268/1; 328/3
C;Superfamily: actin
C;Keywords: acetylated amino end; cell motility; cytoskeleton; methylated amino acid; mi
F;2-375/Product: actin beta #status predicted <WAT>
F;2/Modified site: acetylated amino end (Asp) (in mature form) #status predicted
F;73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 74; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTPTAMYVAIQAVL 15
|||||
Db 126 TTTPTAMYVAIQAVL 140

RESULT 14
AIDO
actin - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: A93223; A92871; S67999; A03004
R;Vandekerckhove, J.; Weber, K.
Nature 284, 475-477, 1980
A;Title: Vegetative Dictyostelium cells containing 17 actin genes express a single major
A;Reference number: A93223; MUID:80143270; PMID:6892652
A;Accession: A93223

A;Molecule type: protein
A;Residues: 1-375 <VAN>
A;Cross-references: UNIPROT:P02577
R;McKewen, M.; Firtel, R.A.
J. Mol. Biol. 151, 593-606, 1981
A;Title: Evidence for sub-families of actin genes in Dictyostelium as determined by comp
A;Reference number: A92871; MUID:82122583; PMID:6276562
A;Accession: A92871
A;Molecule type: mRNA; DNA
A;Residues: 288-375 <WCK>
R;Jungbluth, A.; Eckerskorn, C.; Gerisch, G.; Lottspeich, F.; Stocker, S.; Schweiger, A.
FEBS Lett. 375, 87-90, 1995
A;Title: Stress-induced tyrosine phosphorylation of actin in Dictyostelium cells and loc
A;Reference number: S67999; MUID:96087090; PMID:7498488
A;Accession: S67999
A;Molecule type: protein
A;Residues: 51-61 <JUN>
C;Comment: Although Dictyostelium may contain 17 actin genes, only one major actin is ex;
C;Superfamily: actin
C;Keywords: methylated amino acid
F;73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 74; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTPTAMYVAIQAVL 15
|||||
Db 126 TTTPTAMYVAIQAVL 140

RESULT 15
ATHUB
actin beta - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: A25168; A37248; S23707; A37247; I39394; S38782; A02999
R;Nakajima-Iijima, S.; Hamada, H.; Reddy, P.; Kakunaga, T.
Proc. Natl. Acad. Sci. U.S.A. 82, 6133-6137, 1985
A;Title: Molecular structure of the human cytoplasmic beta-actin gene: interspecies homo
A;Reference number: A25168; MUID:85298307; PMID:2994062
A;Accession: A25168
A;Molecule type: DNA
A;Residues: 1-375 <NKA>
A;Cross-references: UNIPROT:P60709; GB:M10277; NID:g177967; PIDN:AAA51567.1; PID:g177968
A;Note: the authors translated the codon CAG for residue 137 as Glu
R;Ng, S.Y.; Gunning, P.; Eddy, R.; Ponte, P.; Leavitt, J.; Shows, T.; Keddes, L.
Mol. Cell. Biol. 5, 2720-2732, 1985
A;Title: Evolution of the functional human beta-actin gene and its multi-pseudogene fami
A;Reference number: A37248; MUID:86284634; PMID:3837182
A;Accession: A37248
A;Molecule type: mRNA
A;Residues: 1-375 <NGX>
A;Cross-references: EMBL:X00351; DBJ:J00074; GB:M10278; NID:g28251; PIDN:CAA25099.1; PI
A;Note: The human genome contains one functional beta-actin gene and a number of processi
R;Ponte, P.; Ng, S.Y.; Engel, J.; Gunning, P.; Keddes, L.
Nucleic Acids Res. 12, 1687-1696, 1984
A;Title: Evolutionary conservation in the untranslated regions of actin mRNAs: DNA sequ
A;Reference number: S23707; MUID:84144061; PMID:6322116
A;Accession: S23707
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-375 <PON>
A;Cross-references: EMBL:X63432; NID:g28335; PIDN:CAA45026.1; PID:g28336
R;Hanukoglu, I.; Tanese, N.; Fuchs, E.
J. Mol. Biol. 163, 673-678, 1983
A;Title: Complementary DNA sequence of a human cytoplasmic actin. Interspecies divergenc
A;Reference number: A37247; MUID:83189093; PMID:6842590
A;Accession: A37247
A;Molecule type: mRNA
A;Residues: 252-375 <HAN>
A;Cross-references: EMBL:V00478; NID:g28244; PIDN:CAA23745.1; PID:g825616
R;Gunning, P.; Ponte, P.; Okayama, H.; Engel, J.; Blau, H.; Keddes, L.

Mol. Cell. Biol. 3, 787-795, 1983
A:Title: Isolation and characterization of full-length cDNA clones for human alpha-, beta- and gamma-actin
A:Reference number: I39394; MUID:83244575; PMID:6865942
A:Accession: I39394
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-17 <GUN>
A:Cross-references: GB:K00790; NID:gl78031; PIDN:AAA51578.1; PID:gl78032
R:Ohmuri, H.
submitted to the EMBL Data Library, October 1991
A:Reference number: S38782
A:Accession: S38782
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-138, 'M', 140-294, 'D', 296-375 <OHM>
A:Cross-references: EMBL:X63432; NID:g28335; PIDN:CAA5026.1; PID:g28336
C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins, alpha-actinin-1 and alpha-actinin-2.
C:Genetics:
A:Gene: GDB:ACTB
A:Cross-references: GDB:118964; OMIM:102630
A:Map position: 7p22-7p22
A:Introns: 41/3; 121/3; 268/1; 328/3
C:Superfamily: actin
C:Keywords: cell motility; cytoskeleton; methylated amino acid; microfilament; mitosis; F-actin
F:2-375/Product: actin beta #status predicted <MAT>
F:73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 74; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTTPMYVVAIQAVL 15
|||||
Db 126 TTTTTPMYVVAIQAVL 140

Search completed: April 8, 2005, 10:53:05
Job time : 9.3333 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 57.8667 Seconds
(without alignments)
132.739 Million cell updates/sec

Title: US-09-423-351C-6
Perfect score: 74
Sequence: 1 TFNTPAMVAIQAVL 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	58	Q28242	cervus elap
2	74	100.0	60	Q18B1	tubifex tub
3	74	100.0	60	Q18C0	thelohanel
4	74	100.0	60	Q18C2	myxobolus e
5	74	100.0	60	Q18C3	myxobolus e
6	74	100.0	60	Q18C4	myxobolus m
7	74	100.0	60	Q18C5	myxobolus s
8	74	100.0	60	Q18C6	myxobolus i
9	74	100.0	68	Q6UB7	sparus aura
10	74	100.0	95	Q18R2	spodoptera
11	74	100.0	97	Q9JLX9	rattus norv
12	74	100.0	109	Q28916	macaca fusc
13	74	100.0	117	Q8T6P7	elysia chlo
14	74	100.0	117	Q80012	hyala japoni
15	74	100.0	117	Q80013	hyala japoni
16	74	100.0	122	Q94IA3	phaeodactylus v
17	74	100.0	125	Q802E1	zoarces viv
18	74	100.0	125	Q802E2	pachycara b
19	74	100.0	130	Q865G0	capra hircu
20	74	100.0	130	Q865G0	coryphaenoi
21	74	100.0	130	Q865G0	stizostedion
22	74	100.0	132	Q8IA84	ageniaspis
23	74	100.0	133	Q804L7	ageniaspis
24	74	100.0	133	Q804L9	ixodes scap
25	74	100.0	136	Q95V64	ixodes scap
26	74	100.0	144	Q90YX9	fundulus he
27	74	100.0	145	Q91L42	trebouxia j
28	74	100.0	147	Q7X9B5	fragaria an
29	74	100.0	150	Q68AX1	cynops pyrri
30	74	100.0	157	Q96443	glycine max
31	74	100.0	160	Q8T6A7	trichinella
32	74	100.0	160	Q9NAS3	blattella g

32	74	100.0	162	2	Q6UBA0	chelonio my
33	74	100.0	165	2	Q8QFS7	scyllorhinu
34	74	100.0	170	2	Q9NB01	metridium s
35	74	100.0	171	2	Q7XAK3	asparagus o
36	74	100.0	171	2	Q8JH59	chelydra se
37	74	100.0	173	2	Q8RX10	ficus caric
38	74	100.0	174	2	Q819W1	biomphalari
39	74	100.0	174	2	Q819W2	biomphalari
40	74	100.0	174	2	Q819W3	biomphalari
41	74	100.0	174	2	Q819W4	biomphalari
42	74	100.0	174	2	Q819W5	biomphalari
43	74	100.0	174	2	Q819W6	helisoma an
44	74	100.0	174	2	Q819W7	helisoma tr
45	74	100.0	174	2	Q819W8	biomphalari

ALIGNMENTS

RESULT 1						
Q28242	ID	Q28242	PRELIMINARY;	PRT;	58 AA.	
AC	Q28242;					
DT	01-NOV-1996	(Tremblrel. 01, Created)				
DT	01-JUN-2003	(Tremblrel. 24, Last annotation update)				
DE	Actin, cytoplasmic 1 (Beta-actin) (Fragment).					
GN	Name=ACTB;					
OS	Cervus elaphus (Red deer).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;					
OC	Cervinae; Cervus.					
OX	NCBI_TaxID=9860;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=Antler;					
RX	MEDLINE=98233260; PubMed=9571767;					
RX	DOI=10.1002/(SICI)1097-010X(19980501)281:1<36::AID-JE26>3.0.CO;2-D;					
RA	Francis S.M., Suttie J.M.;					
RT	"Detection of growth factors and proto-oncogene mRNA in the growing tip of red deer (Cervus elaphus) antler using reverse-transcriptase polymerase chain reaction (RT-PCR).";					
RT	J. Exp. Zool. 281:36-42(1998).					
RL	-!- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells.					
CC	-!- SUBUNIT: Polymerization of globular actin (G-actin) leads to a structural filament (F-actin) in the form of a two-stranded helix. Each actin can bind to 4 others.					
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic.					
CC	-!- MISCELLANEOUS: In vertebrates 3 main groups of actin isoforms, alpha, beta and gamma have been identified. The alpha actins are found in muscle tissues and are a major constituent of the contractile apparatus. The beta and gamma actins co-exist in most cell types as components of the cytoskeleton and as mediators of internal cell motility.					
CC	-!- SIMILARITY: Belongs to the actin family.					
DR	EMBL; U62112; AB05258.1; -.					
DR	HSSP; P02577; INMI.					
DR	GO; GO:0015629; C:actin cytoskeleton; IEA.					
DR	GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.					
DR	InterPro; IPR004001; Actin.					
DR	InterPro; IPR004000; Actin_like.					
DR	Pfam; PF00022; Actin; 1.					
DR	PROSITE; PS00406; ACTINS_1; PARTIAL.					
DR	PROSITE; PS00432; ACTINS_2; PARTIAL.					
DR	PROSITE; PS01132; ACTINS_ACT LIKE; PARTIAL.					
KW	Cytoskeleton; Multigene family; Structural protein.					
FT	NON TER 1					
FT	CHAIN <1> >58 ACTIN, CYTOPLASMIC 1.					
FT	NON TER 58					
SEQUENCE	58 AA; 6290 MW; 26D0D8BEC629A61 CRC64;					

```
Query Match      100.0%; Score 74; DB 2; Length 58;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPMYVAIQAVL 15
Db 7 TFNTPMYVAIQAVL 21

RESULT 2
Q818B1
ID Q818B1 PRELIMINARY; PRT; 60 AA.
AC Q818B1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative beta-actin (Fragment).
OS Tubifex tubifex (Sludge worm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Tubificina; Tubificidae; Tubifex.
OX NCBI_TaxID=6396;
RN [1]
RP SEQUENCE FROM N.A.
RA Kelley G.O., Beauchamp K.A., Hedrick R.R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AY157023; AAN85108.1; -.
DR HSSP; P02568; 1MA9.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON_TER 1 60
FT NON_TER 60 60
SQ SEQUENCE 60 AA; 6591 MW; 8127546708884838 CRC64;

Query Match      100.0%; Score 74; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPMYVAIQAVL 15
Db 26 TFNTPMYVAIQAVL 40

RESULT 3
Q818C0
ID Q818C0 PRELIMINARY; PRT; 60 AA.
AC Q818C0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative beta-actin (Fragment).
OS Theohanelius nikolskii.
OC Eukaryota; Metazoa; Myxozoa; Myxosporia; Bivalvulida; Platysporina;
OC Myxobolidae; Theohanelius.
OX NCBI_TaxID=215725;
RN [1]
RP SEQUENCE FROM N.A.
RA Kelley G.O., Beauchamp K.A., Hedrick R.R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AY157014; AAN85099.1; -.
DR HSSP; P02577; 1NN1.

Query Match      100.0%; Score 74; DB 2; Length 58;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPMYVAIQAVL 15
Db 26 TFNTPMYVAIQAVL 40

RESULT 4
Q818C2
ID Q818C2 PRELIMINARY; PRT; 60 AA.
AC Q818C2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative beta-actin (Fragment).
OS Myxobolus episcuamalis.
OC Eukaryota; Metazoa; Myxozoa; Myxosporia; Bivalvulida; Platysporina;
OC Myxobolidae; Myxobolus.
OX NCBI_TaxID=204748;
RN [1]
RP SEQUENCE FROM N.A.
RA Kelley G.O., Beauchamp K.A., Hedrick R.R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AY157012; AAN85097.1; -.
DR HSSP; P02577; 1NN1.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON_TER 1 60
FT NON_TER 60 60
SQ SEQUENCE 60 AA; 6484 MW; 3D93D5A1D3D424A7 CRC64;

Query Match      100.0%; Score 74; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPMYVAIQAVL 15
Db 26 TFNTPMYVAIQAVL 40

RESULT 5
Q818C3
ID Q818C3 PRELIMINARY; PRT; 60 AA.
AC Q818C3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative beta-actin (Fragment).
OS Myxobolus exiguus.
OC Eukaryota; Metazoa; Myxozoa; Myxosporia; Bivalvulida; Platysporina;
OC Myxobolidae; Myxobolus.
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DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON_TER 1 60
FT NON_TER 60 60
SQ SEQUENCE 60 AA; 6498 MW; 3983D5A1D3D424A7 CRC64;

Query Match      100.0%; Score 74; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPMYVAIQAVL 15
Db 26 TFNTPMYVAIQAVL 40

RESULT 4
Q818C2
ID Q818C2 PRELIMINARY; PRT; 60 AA.
AC Q818C2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative beta-actin (Fragment).
OS Myxobolus episcuamalis.
OC Eukaryota; Metazoa; Myxozoa; Myxosporia; Bivalvulida; Platysporina;
OC Myxobolidae; Myxobolus.
OX NCBI_TaxID=204748;
RN [1]
RP SEQUENCE FROM N.A.
RA Kelley G.O., Beauchamp K.A., Hedrick R.R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AY157012; AAN85097.1; -.
DR HSSP; P02577; 1NN1.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON_TER 1 60
FT NON_TER 60 60
SQ SEQUENCE 60 AA; 6484 MW; 3D93D5A1D3D424A7 CRC64;

Query Match      100.0%; Score 74; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPMYVAIQAVL 15
Db 26 TFNTPMYVAIQAVL 40

RESULT 5
Q818C3
ID Q818C3 PRELIMINARY; PRT; 60 AA.
AC Q818C3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative beta-actin (Fragment).
OS Myxobolus exiguus.
OC Eukaryota; Metazoa; Myxozoa; Myxosporia; Bivalvulida; Platysporina;
OC Myxobolidae; Myxobolus.
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OX NCBI_TaxID=204750;
RN [1]
RP SEQUENCE FROM N.A.
RA Kelley G.O., Beauchamp K.A., Hedrick R.R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AY157011; AAN85096.1; -.
DR HSSP; P02577; 1NM1.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
FT NON_TER 1 60
FT NON_TER 60 60
SQ SEQUENCE 60 AA; 6532 MW; C383DFABD3D424AA CRC64;

Query Match 100.0%; Score 74; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPMYVAIQAVL 15
Db 26 TFNTPMYVAIQAVL 40

RESULT 6
Q818C4
ID Q818C4 PRELIMINARY; PRT; 60 AA.
AC Q818C4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative beta-actin (Fragment).
OS Myxobolus muelleri.
OC Eukaryota; Metazoa; Myxozoa; Myxosporina; Bivalvulida; Platysoptina;
OC Myxobolidae; Myxobolus.
OX NCBI_TaxID=204749;
RN [1]
RP SEQUENCE FROM N.A.
RA Kelley G.O., Beauchamp K.A., Hedrick R.R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AY157010; AAN85095.1; -.
DR HSSP; P02577; 1NM1.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
FT NON_TER 1 60
FT NON_TER 60 60
SQ SEQUENCE 60 AA; 6498 MW; 3983D5A1D3D424A7 CRC64;

Query Match 100.0%; Score 74; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPMYVAIQAVL 15
Db 26 TFNTPMYVAIQAVL 40

RESULT 7
Q818C6
ID Q818C6 PRELIMINARY; PRT; 60 AA.
AC Q818C6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative beta-actin (Fragment).
OS Myxobolus insidiosus.
OC Eukaryota; Metazoa; Myxozoa; Myxosporina; Bivalvulida; Platysoptina;
OC Myxobolidae; Myxobolus.
OX NCBI_TaxID=59784;
RN [1]
RP SEQUENCE FROM N.A.
RA Kelley G.O., Beauchamp K.A., Hedrick R.R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AY157008; AAN85093.1; -.
DR HSSP; P02577; 1NM1.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
FT NON_TER 1 60
FT NON_TER 60 60
SQ SEQUENCE 60 AA; 6468 MW; 1483D5A1D3D424B0 CRC64;

Query Match 100.0%; Score 74; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPMYVAIQAVL 15
Db 26 TFNTPMYVAIQAVL 40

RESULT 7
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Q818C5
ID Q818C5 PRELIMINARY; PRT; 60 AA.
AC Q818C5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative beta-actin (Fragment).
OS Myxobolus spinacurvatura.
OC Eukaryota; Metazoa; Myxozoa; Myxosporina; Bivalvulida; Platysoptina;
OC Myxobolidae; Myxobolus.
OX NCBI_TaxID=182349;
RN [1]
RP SEQUENCE FROM N.A.
RA Kelley G.O., Beauchamp K.A., Hedrick R.R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AY157009; AAN85094.1; -.
DR HSSP; P02577; 1NM1.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
FT NON_TER 1 60
FT NON_TER 60 60
SQ SEQUENCE 60 AA; 6498 MW; 3983D5A1D3D424A7 CRC64;

Query Match 100.0%; Score 74; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPMYVAIQAVL 15
Db 26 TFNTPMYVAIQAVL 40

RESULT 8
Q818C6
ID Q818C6 PRELIMINARY; PRT; 60 AA.
AC Q818C6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative beta-actin (Fragment).
OS Myxobolus insidiosus.
OC Eukaryota; Metazoa; Myxozoa; Myxosporina; Bivalvulida; Platysoptina;
OC Myxobolidae; Myxobolus.
OX NCBI_TaxID=59784;
RN [1]
RP SEQUENCE FROM N.A.
RA Kelley G.O., Beauchamp K.A., Hedrick R.R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AY157008; AAN85093.1; -.
DR HSSP; P02577; 1NM1.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
FT NON_TER 1 60
FT NON_TER 60 60
SQ SEQUENCE 60 AA; 6468 MW; 1483D5A1D3D424B0 CRC64;
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Query Match      100.0%; Score 74; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPMYVAIQAVL 15
Db 26 TFNTPMYVAIQAVL 40

RESULT 9
Q6USB7      PRELIMINARY;      PRT;      68 AA.
AC Q6USB7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Beta-actin (Fragment).
OS Sparus aurata (Gilthead sea bream).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Sparus.
OX NCBI_TaxID=8175;
RN [1]
RP SEQUENCE FROM N.A.
RA Krey G.D., Boukouvla E., Hondrogiannis C.I., Theodoridou M.D.,
RA Kalevra V.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AY362763; AAO56183.1; -.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON TER 68
FT NON TER 68
SQ SEQUENCE 68 AA; 7935 MW; 66E08E30906782D CRC64;

Query Match      100.0%; Score 74; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPMYVAIQAVL 15
Db 50 TFNTPMYVAIQAVL 64

RESULT 10
Q8ISR2      PRELIMINARY;      PRT;      95 AA.
AC Q8ISR2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Actin (Fragment).
OS Spodoptera frugiperda (Fall armyworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Amphipyrae; Spodoptera.
OX NCBI_TaxID=7108;
RN [1]
RP SEQUENCE FROM N.A.
RA Nobiron I., O'Reilly D.R., Olszewski J.A.;
RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).

-!- SIMILARITY: Belongs to the actin family.
EMBL; AF548015; AAN38748.1; -.
HSSP; P02577; INWI
GO; GO:0015629; C:actin cytoskeleton; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004000; Actin_like.
PFam; PF00022; Actin; 1.
PRINTS; PR00190; ACTIN.
PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
Structural protein.
NON TER 1
NON TER 95
SEQUENCE 95 AA; 10656 MW; E0C697FD09770932 CRC64;

Query Match      100.0%; Score 74; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 8.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPMYVAIQAVL 15
Db 46 TFNTPMYVAIQAVL 60

RESULT 11
Q9JLX9      PRELIMINARY;      PRT;      97 AA.
AC Q9JLX9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta actin (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Sprague-Dawley;
RA Toporsian M., Auer G., Zacour M., Cernacek P., Ward M.E.;
RA Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
EMBL; AF122902; AAF31761.1; -.
HSSP; P02577; INWI.
GO; GO:0015629; C:actin cytoskeleton; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004000; Actin_like.
PFam; PF00022; Actin; 1.
PRINTS; PR00190; ACTIN.
PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
Structural protein.
NON TER 1
NON TER 97
SEQUENCE 97 AA; 11014 MW; D5CE6E9964444EF9 CRC64;

Query Match      100.0%; Score 74; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPMYVAIQAVL 15
Db 59 TFNTPMYVAIQAVL 73

RESULT 12
Q28916      PRELIMINARY;      PRT;      109 AA.
AC Q28916;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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DE Actin (Fragment).
OS Macaca fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Macaca.
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9542;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96071113; PubMed=7577717; DOI=10.1016/0960-0760(95)00157-U;
RA Yamada-Mouri N., Hirata S., Hayashi M., Kato J.;
RT "Analysis of the expression and the first exon of aromatase mRNA in
monkey brain";
RL J. Steroid Biochem. Mol. Biol. 55:17-23 (1995).
DR EMBL; S79782; AAB35618.2; -;
DR HSSP; P10983; 1D4X.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; F:structural constituent of cytoskeleton; IEA.
DR Pfam; PF00022; Actin; 1.
FT NON TER 1
FT NON TER 109
SQ SEQUENCE 109 AA; 12333 MW; 64A64E108CDDA54C CRC64;
Query Match 100.0%; Score 74; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPMYVAIOAVL 15
Db 11 TFNTPMYVAIOAVL 25

RESULT 13

ID Q876P7 PRELIMINARY; PRT; 117 AA.
AC Q876P7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Actin (Fragment).
OS Elysia chlorotica (Sea slug).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia;
OC Sacoglossa; Elysioidea; Elysidae; Elysia.
OX NCBI_TaxID=188477;
RN [1]
RP SEQUENCE FROM N.A.
RA Fukao T., Summer E.J., Rumpho M.E.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AF448493; AAL87639.1; -;
DR HSSP; P02577; 1NM1.
DR GO; GO:0005884; C:actin filament; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004001; Actin.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS00406; ACTINS_1; 1.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON TER 1
FT NON TER 117
SQ SEQUENCE 117 AA; 13270 MW; C5D4DAFDF95F03AC CRC64;
Query Match 100.0%; Score 74; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPMYVAIOAVL 15
Db 91 TFNTPMYVAIOAVL 105

RESULT 14

Q80012
ID Q80012 PRELIMINARY; PRT; 117 AA.
AC Q80012;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-actin 2 (Fragment).
GN Name=ACTB2;
OS Hyla japonica (Japanese tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylinae;
OC Hyla.
OX NCBI_TaxID=109175;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Kohno S., Kamishima Y., Iguchi T.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AB092520; BAC66208.1; -;
DR HSSP; P60712; 1HLU.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON TER 1
FT NON TER 117
SQ SEQUENCE 117 AA; 13291 MW; 64C6BAC4F84184CF CRC64;
Query Match 100.0%; Score 74; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPMYVAIOAVL 15
Db 47 TFNTPMYVAIOAVL 61

RESULT 15

Q80013
ID Q80013 PRELIMINARY; PRT; 117 AA.
AC Q80013;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-actin 1 (Fragment).
GN Name=ACTB1;
OS Hyla japonica (Japanese tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylinae;
OC Hyla.
OX NCBI_TaxID=109175;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Kohno S., Kamishima Y., Iguchi T.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.

DR EMBL; AB092519; BAC66207.1; -.
 DR HSSP; P60712; 1HU.
 DR GO; GO:0015629; C:actin cytoskeleton; IEA.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
 DR InterPro; IPR004000; Actin_like.
 DR Pfam; PF00022; Actin; 1.
 DR PRINTS; PR00190; ACTIN.
 DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
 KW Structural protein.
 FT NON_TER 1
 FT NON_TER 117
 SQ SEQUENCE 117 AA; 13291 MW; 64C6BAC4F84184CF CRC64;

Query Match 100.0%; Score 74; DB 2; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFNTPAMYVAIQAVL 15
 |||||
 Db 47 TFNTPAMYVAIQAVL 61

Search completed: April 8, 2005, 12:03:09
 Job time : 58.8667 secs

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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 62.4 Seconds
(without alignments)
92.971 Million cell updates/sec

Title: US-09-423-351C-7

Perfect score: 75

Sequence: 1 LPHAILRLDLAARDL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	100.0	15	2 AAW92533	Beta-acti
2	75	100.0	97	4 AAM13687	Peptide #
3	75	100.0	97	4 ABB32618	Peptide #
4	75	100.0	97	4 AAM26087	Peptide #
5	75	100.0	97	4 ABB27467	Human pep
6	75	100.0	97	4 ABB18116	Protein #
7	75	100.0	97	4 AAM65825	Human bon
8	75	100.0	97	4 AAM53448	Human bra
9	75	100.0	97	4 ABB47471	Human liv
10	75	100.0	97	4 AAM01437	Peptide #
11	75	100.0	97	5 ABB35459	Human pep
12	75	100.0	118	3 AAG26468	Arabidops
13	75	100.0	135	3 AAG26467	Arabidops
14	75	100.0	148	5 ADK36534	Novel hum
15	75	100.0	150	4 ABB15101	Novel hum
16	75	100.0	153	4 ABB15497	Novel hum
17	75	100.0	168	5 ABB42912	Human ova
18	75	100.0	196	6 ABB70816	Human adi
19	75	100.0	211	7 ABB73899	DNA clone
20	75	100.0	229	3 AAG38700	Arabidops
21	75	100.0	246	3 AAG38699	Arabidops
22	75	100.0	257	3 AAG37992	Arabidops
23	75	100.0	257	3 AAG20916	Arabidops
24	75	100.0	274	6 ABB70549	Human adi
25	75	100.0	276	3 AAG50947	Arabidops

26	75	100.0	277	3 AAG05115	Arabidops
27	75	100.0	294	3 AAG20915	Arabidops
28	75	100.0	294	3 AAG37991	Arabidops
29	75	100.0	294	7 ADI63068	Human apo
30	75	100.0	295	3 AAG20914	Arabidops
31	75	100.0	295	3 AAG37990	Arabidops
32	75	100.0	304	3 AAG50946	Arabidops
33	75	100.0	305	3 AAG05114	Arabidops
34	75	100.0	308	3 AAG37210	Arabidops
35	75	100.0	311	3 AAG37209	Arabidops
36	75	100.0	321	3 AAG50945	Arabidops
37	75	100.0	322	3 AAG05113	Arabidops
38	75	100.0	332	3 AAG06448	Arabidops
39	75	100.0	332	3 AAG30774	Arabidops
40	75	100.0	332	3 AAG50873	Arabidops
41	75	100.0	332	3 AAG07390	Arabidops
42	75	100.0	332	3 AAG41511	Arabidops
43	75	100.0	332	3 AAG37989	Arabidops
44	75	100.0	332	3 AAG37317	Arabidops
45	75	100.0	332	3 AAG44697	Zea mays

ALIGNMENTS

RESULT 1

AAW92533
ID AAW92533 standard; peptide; 15 AA.

AC AAW92533;

DT 26-APR-1999 (first entry)

DE Beta-actin reference peptide substrate #7.

KW Peptide substrate; CCT; eukaryotic type II chaperonin complex; cyclin; binding agent; substrate-binding site; SBS; substrate folding; actin; tubulin; treatment; cancer; anticancer drug; viral infection; screening; reduced toxicity.

OS Synthetic.

PN WO9853322-A1.

PD 26-NOV-1998.

PF 22-MAY-1998; 98WO-GB001485.

PR 23-MAY-1997; 97GB-00010762.

PA (CANC-) INST CANCER RES ROYAL CANCER HOSPITAL.

PI Willison K, Hynes G, Liou AK;

WP1; 1999-070162/06.

Identifying specific binding agents for substrate binding site in CCT chaperonin complex - also new peptide binding agents and their mimetics, and peptides containing a specific CCT binding site, used for treating cancer.

Disclosure; Fig 10; 97pp; English.

This invention describes a method which uses the CCT (eukaryotic type II chaperonin) complex or part of it, for identifying a binding agent that can occupy a substrate-binding site (SBS) on the CCT complex. By binding to the CCT complex, the binding agents block an SBS so that biological activity of the CCT complex is affected, particularly its ability to fold substrates such as actin, tubulin and cyclin. The binding agents are useful for treatment of cancer, particularly when used in combination with an anticancer drug, or viral infections. Nucleic acid fragments are used to screen for agents, e.g. binding agents that modulate interaction between the CCT complex and a protein that is to be folded. The binding

CC agents may target cells that are actively synthesising tubulin etc.
CC (unlike known microtubule-stabilising agents that affect all cells), so
CC should have reduced toxicity for normal cells. AAW92527-W92541 are
CC peptide substrates used in the method of the invention
XX
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 75; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLAGRDL 15
Db 1 LPHAILRLDLAGRDL 15
|||||

RESULT 2
AAM13687
ID AAM13687 standard; protein; 97 AA.

XX
AC AAM13687;

XX
DT 12-OCT-2001 (first entry)

XX Peptide #121 encoded by probe for measuring cervical gene expression.

XX Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer.

XX
OS Homo sapiens.

XX WO200157278-A2.

XX
PD 09-AUG-2001.

XX
PF 30-JAN-2001; 2001WO-US000670.

XX
PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX
FA (MOLE-) MOLECULAR DYNAMICS INC.

XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX
DR WPI; 2001-488901/53.

XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human cervical epithelial cells.

XX
PS Claim 27; SEQ ID NO 18513; 487pp; English.

XX
CC The present invention relates to human single exon nucleic acid probes
CC (SENPs: see AAI10068-AA128459). The present sequence is a peptide encoded
CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
CC can be used to produce a single exon microarray, which can be used for
CC measuring human gene expression in a sample derived from human cervical
CC epithelial cells. By measuring gene expression, the probes are therefore
CC useful in grading and/or staging of diseases of the cervix, notably
CC cervical cancer. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 97 AA;

Query Match 100.0%; Score 75; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLAGRDL 15
Db 50 LPHAILRLDLAGRDL 64
|||||

RESULT 3
ABB32618

ID ABB32618 standard; peptide; 97 AA.

XX
AC ABB32618;

XX
DT 04-FEB-2002 (first entry)

XX Peptide #124 encoded by human foetal liver single exon probe.

XX Human; foetal liver; gene expression; single exon nucleic acid probe.

XX
OS Homo sapiens.

XX WO200157277-A2.

XX
PD 09-AUG-2001.

XX
PF 30-JAN-2001; 2001WO-US000669.

XX
PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX
FA (MOLE-) MOLECULAR DYNAMICS INC.

XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX
DR WPI; 2001-483447/52.

XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.

XX
PS Claim 27; SEQ ID NO 25253; 639pp + Sequence Listing; English.

XX
CC The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 97 AA;

Query Match 100.0%; Score 75; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLAGRDL 15
Db 50 LPHAILRLDLAGRDL 64
|||||

RESULT 4
AAM26087

ID AAM26087 standard; protein; 97 AA.

XX
AC AAM26087;

XX
DT 17-OCT-2001 (first entry)

XX Peptide #124 encoded by probe for measuring placental gene expression.

XX Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.
KW Homo sapiens.

OS

XX WO200157272-A2.

PN

XX PD

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000663.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human placenta.

XX Claim 27; SEQ ID NO 26356; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENP;

XX see AAT31315-AA157546). The present sequence is a peptide encoded by one

XX such probe. The probes are useful for producing a microarray for

XX predicting, measuring and displaying gene expression in samples derived

XX from human placenta. The probes are useful for antenatal diagnosis of

XX human genetic disorders

XX Sequence 97 AA;

Query Match 100.0%; Score 75; DB 4; Length 97;

Best Local Similarity 100.0%; Pred. No. 2.1e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLAAGRD 15

Db 50 LPHAILRLDLAAGRD 64

RESULT 5

ABB27467

ID ABB27467 standard; peptide; 97 AA.

XX

AC ABB27467;

XX

XX 01-FEB-2002 (first entry)

XX Human peptide #118 encoded by breast cell single exon nucleic acid probe.

XX Human; microarray; single exon probe; gene expression; breast; disease;

XX cancer.

XX Homo sapiens.

XX WO200157271-A2.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-496933/54.

XX New spatially-addressable set of single exon nucleic acid probes, useful

XX for measuring gene expression in sample derived from human breast,

XX comprises number of single exon nucleic acid probes.

XX Claim 27; SEQ ID NO 10435; 327pp + Sequence Listing; English.

XX The invention relates to a spatially-addressable set of single exon

XX nucleic acid probes for measuring gene expression in a sample derived

XX from human breast and BT 474 cells. The method involves contacting the

XX probes with a collection of detectably labelled nucleic acids derived

XX from mRNA of human breast, and then measuring the label bound to each

XX probe of the microarray. The probes are useful for verifying the

XX expression of regions of genomic DNA predicted to encode proteins. They

XX are useful for gene discovery, and for determining predisposition and/or

XX assessing breast disease. Gene expression analysis is useful for

XX this invention presents a far greater diversity of probes for measuring

XX gene expression, with far less bias than expressed sequence tag

XX microarrays. The method is suitable for rapid production of functional

XX information from genomic sequence. The present sequence is a peptide

XX encoded by a single exon nucleic acid probe of the invention. Note: The

XX sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from WIPO

XX at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 97 AA;

Query Match 100.0%; Score 75; DB 4; Length 97;

Best Local Similarity 100.0%; Pred. No. 2.1e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLAAGRD 15

Db 50 LPHAILRLDLAAGRD 64

RESULT 6

ABB18116

ID ABB18116 standard; protein; 97 AA.

XX

AC ABB18116;

XX

XX 23-JAN-2002 (first entry)

XX Protein #115 encoded by probe for measuring heart cell gene expression.

XX Human; gene expression; heart; microarray; vascular system;

XX cardiovascular disease; hypertension; cardiac arrhythmia;

XX congenital heart disease.

XX Homo sapiens.

XX WO200157272-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000666.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human placenta.

XX Claim 27; SEQ ID NO 26356; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENP;

XX see AAT31315-AA157546). The present sequence is a peptide encoded by one

XX such probe. The probes are useful for producing a microarray for

XX predicting, measuring and displaying gene expression in samples derived

XX from human placenta. The probes are useful for antenatal diagnosis of

XX human genetic disorders

XX Sequence 97 AA;

Query Match 100.0%; Score 75; DB 4; Length 97;

Best Local Similarity 100.0%; Pred. No. 2.1e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLAAGRD 15

Db 50 LPHAILRLDLAAGRD 64

RESULT 6

ABB18116

ID ABB18116 standard; protein; 97 AA.

XX

AC ABB18116;

XX

XX 23-JAN-2002 (first entry)

XX Protein #115 encoded by probe for measuring heart cell gene expression.

XX Human; gene expression; heart; microarray; vascular system;

XX cardiovascular disease; hypertension; cardiac arrhythmia;

XX congenital heart disease.

XX Homo sapiens.

XX WO200157274-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000666.

XX 04-FEB-2000; 2000US-0180312P.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human placenta.

XX Claim 27; SEQ ID NO 26356; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENP;

XX see AAT31315-AA157546). The present sequence is a peptide encoded by one

XX such probe. The probes are useful for producing a microarray for

XX predicting, measuring and displaying gene expression in samples derived

XX from human placenta. The probes are useful for antenatal diagnosis of

XX human genetic disorders

XX Sequence 97 AA;

Query Match 100.0%; Score 75; DB 4; Length 97;

Best Local Similarity 100.0%; Pred. No. 2.1e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLAAGRD 15

Db 50 LPHAILRLDLAAGRD 64

RESULT 5

ABB27467

ID ABB27467 standard; peptide; 97 AA.

XX

AC ABB27467;

XX

XX 01-FEB-2002 (first entry)

XX Human peptide #118 encoded by breast cell single exon nucleic acid probe.

XX Human; microarray; single exon probe; gene expression; breast; disease;

XX cancer.

XX Homo sapiens.

XX WO200157271-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000662.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

```

PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488999/53.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT hearts.
XX
PS Claim 15; SEQ ID NO 19886; 530pp; English.
XX
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart (see
CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
CC probe. The probes may be used for predicting, measuring and displaying
CC gene expression in samples derived from the human heart via microarrays.
CC By measuring gene expression, the probes are useful for predicting,
CC diagnosing, grading, staging, monitoring and prognosing diseases of the
CC human heart and vascular system e.g. cardiovascular disease,
CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 97 AA;

Query Match 100.0%; Score 75; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPFAILRLDLGRDL 15
Db 50 LPFAILRLDLGRDL 64

RESULT 7
AAM65825
ID AAM65825 standard; protein; 97 AA.
XX
AC AAM65825;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 26131.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma.
XX
OS Homo sapiens.
XX
PN WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US0000668.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488900/53.
XX

XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human bone marrow.
XX
XX Example 4; SEQ ID NO 26131; 658pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX bone marrow. They can be used to measure gene expression in bone marrow
XX samples, which may enable the improved diagnosis and treatment of cancers
XX such as lymphoma, leukaemia and myeloma. The present sequence is a
XX protein encoded by one of the probes of the invention
XX
XX Sequence 97 AA;

Query Match 100.0%; Score 75; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPFAILRLDLGRDL 15
Db 50 LPFAILRLDLGRDL 64

RESULT 8
AAM53448
ID AAM53448 standard; protein; 97 AA.
XX
AC AAM53448;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 25553.
XX
KW Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US0000667.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains.
XX
XX Example 4; SEQ ID NO 25553; 650pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is a protein encoded by one of
XX the probes of the invention
XX
XX Sequence 97 AA;

```

Query Match 100.0%; Score 75; DB 4; Length 97;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLAGRDL 15
 |||||
 Db 50 LPHAILRLDLAGRDL 64

RESULT 9

ID ABG47471 standard; peptide; 97 AA.

AC ABG47471;
 XX
 XX 25-FEB-2003 (first entry)
 DT
 XX Human liver peptide, SEQ ID NO 26119.
 DE
 XX Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
 KW hypercholesterolaemia; coronary heart disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200157273-A2.
 XX
 XX 09-AUG-2001.
 PD
 XX 30-JAN-2001; 2001WO-US000664.
 PP
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.

(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR;

WPI; 2001-488898/53.

Human genome-derived single exon nucleic acid probes useful for analyzing
 gene expression in human adult liver.

Claim 27; SEQ ID NO 26119; 658pp; English.

The invention relates to a single exon nucleic acid probe (SENP) (I) for
 measuring human gene expression in a sample derived from human adult
 liver, comprising one of 13109 defined nucleotide sequences given in the
 specification (or complements/fragments). The probe hybridizes at high
 stringency to a nucleic acid molecule expressed in the human adult liver.
 (I) may be used for predicting, measuring and displaying gene expression
 in samples derived from human adult liver. The genes identified may be
 involved in genetic liver diseases such as cirrhosis,
 hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
 associated with coronary heart disease. ABG47348-ABG5930 represent human
 liver single exon encoded peptides of the invention. Note: The sequence
 information for this patent does not appear in the printed specification
 but was obtained in electronic format directly from WIPO at
 ftp.wipo.int/pub/published_pct_sequences

Sequence 97 AA;

Query Match 100.0%; Score 75; DB 4; Length 97;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLAGRDL 15
 |||||

Db 50 LPHAILRLDLAGRDL 64

RESULT 10

ID AAM01437 standard; protein; 97 AA.

AC AAM01437;
 XX
 XX 09-OCT-2001 (first entry)
 DT

XX Peptide #119 encoded by probe for measuring human breast gene expression.
 DE Probe; human; breast disease; breast cancer; development disorder;
 KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
 XX
 OS Homo sapiens.
 XX
 PN WO200157270-A2.
 XX
 XX 09-AUG-2001.
 PD
 XX 29-JAN-2001; 2001WO-US000661.
 PP
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.

(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR;

WPI; 2001-476286/51.

Novel single exon nucleic acid probe used to measuring gene expression in
 a human breast.

Claim 27; SEQ ID NO 10177; 322pp; English.

The present invention relates to novel single exon nucleic acid probes
 (see AAI00010-AA110067). The present sequence is a peptide encoded by one
 such probe. The probes are useful for measuring human gene expression in
 a human breast sample, where the probe hybridizes at high stringency to a
 nucleic acid expressed in the human breast. The probes are useful for
 predicting, diagnosing, grading, staging, monitoring and prognosing
 diseases of the human breast, particularly those diseases with polygenic
 aetiology. The diseases include: breast cancer, disorders of development,
 inflammatory diseases of the breast, fibrocystic changes, proliferative
 breast disease and non-carcinoma tumours. Note: The sequence data for
 this patent did not form part of the printed specification, but was
 obtained in electronic format directly from WIPO at
 ftp.wipo.int/pub/published_pct_sequences

Sequence 97 AA;

Query Match 100.0%; Score 75; DB 4; Length 97;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLAGRDL 15
 |||||
 Db 50 LPHAILRLDLAGRDL 64

RESULT 11

ID ABG35459 standard; peptide; 97 AA.

AC ABG35459;

XX 19-AUG-2002 (first entry)

DE Human peptide encoded by genome-derived single exon probe SEQ ID 25124.

XX Human; single exon probe; asthma; lung cancer; COPD; ILD;

KW chronic obstructive pulmonary disease; interstitial lung disease;

KW familial idiopathic pulmonary fibrosis; neurofibromatosis;

KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;

KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;

KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;

KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;

KW primary ciliary dyskinesia; pulmonary hypertension;

KW hyaline membrane disease.

XX Homo sapiens.

XX WO200186003-A2.

XX 15-NOV-2001.

XX 30-JAN-2001; 2001WO-US000665.

XX 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2002-114183/15.

XX Spatially-addressable set of single exon nucleic acid probes, used to

PT measure gene expression in human lung samples.

XX Claim 27; SEQ ID NO 25124; 634pp; English.

PS The invention relates to a spatially-addressable set of single exon

CC nucleic acid probes for measuring gene expression in a sample derived

CC from human lung comprising single exon nucleic acid probes having one of

CC 12614 nucleic acid sequences mentioned in the specification, or their

CC complements or the 12387 open reading frames derived from the 12614

CC probes. Also included are a microarray comprising the novel set of probes

CC; the novel set of probes which hybridize at high stringency to a nucleic

CC acid expressed in the human lung; measuring gene expression in a sample

CC derived from human lung, comprising (a) contacting the array with a

CC collection of detectably labeled nucleic acids derived from human lung

CC mRNA, and (b) measuring the label detectably bound to each probe of the

CC array; identifying exons in a eukaryotic genome, comprising (a)

CC algorithmically predicting at least one exon from genomic sequences of

CC the eukaryote; and (b) detecting specific hybridization of detectably

CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,

CC having a fragment identical to the predicted exon, the probe is included

CC in the above mentioned microarray; assigning exons to a single gene,

CC comprising (a) identifying exons from genomic sequence by the method

CC above and (b) measuring the expression of each of the exons in several

CC tissues and/or cell types using hybridization to a single exon

CC microarrays having a probe with the exon, where a common pattern of

CC expression of the exons in the tissues and/or cell types indicates that

CC the exons should be assigned to a single gene; a peptide comprising one

CC of 12011 sequences, mentioned in the specification, or encoded by the

CC probes/open reading frames (ORF). The probes are used for gene expression

CC analysis, and for identifying exons in a gene, particularly using human

CC lung derived mRNA and for the study of lung diseases such as asthma, lung

CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung

CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,

CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-

CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary

CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,

CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary

CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The

CC present sequence is a peptide/protein encoded by a single exon probe of

CC the invention. Note: The sequence data for this patent did not form part

CC of the printed specification, but was obtained in electronic format

CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 97 AA;

Query Match 100.0%; Score 75; DB 5; Length 97;

Best Local Similarity 100.0%; Pred. No. 2.1e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPHAILRLDLAAGDRL 15

DB 50 LPHAILRLDLAAGDRL 64

RESULT 12

AG26468

ID AAG26468 standard; protein; 118 AA.

XX AC AAG26468;

XX 17-OCT-2000 (first entry)

DT DE Arabidopsis thaliana protein fragment SEQ ID NO: 30934.

XX Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.

XX Arabidopsis thaliana.

OS EP1033405-A2.

XX 06-SEP-2000.

PF 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125788P.

PR 25-MAR-1999; 99US-0126284P.

PR 29-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0127462P.

PR 06-APR-1999; 99US-0128234P.

PR 16-APR-1999; 99US-0128714P.

PR 19-APR-1999; 99US-0129845P.

PR 21-APR-1999; 99US-0130077P.

PR 23-APR-1999; 99US-0130449P.

PR 23-APR-1999; 99US-0130510P.

PR 28-APR-1999; 99US-0130891P.

PR 30-APR-1999; 99US-0131449P.

PR 30-APR-1999; 99US-0132048P.

PR 04-MAY-1999; 99US-0132407P.

PR 04-MAY-1999; 99US-0132484P.

PR 05-MAY-1999; 99US-0132485P.

PR 06-MAY-1999; 99US-0132486P.

PR 07-MAY-1999; 99US-0132487P.

PR 11-MAY-1999; 99US-0132863P.

PR 14-MAY-1999; 99US-0134218P.

PR 14-MAY-1999; 99US-0134219P.

PR 14-MAY-1999; 99US-0134221P.

PR 14-MAY-1999; 99US-0134370P.

PR 18-MAY-1999; 99US-0134768P.

PR 19-MAY-1999; 99US-0134941P.

PR 20-MAY-1999; 99US-0135124P.

PR 21-MAY-1999; 99US-0135353P.

PR 24-MAY-1999; 99US-0135629P.


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PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match      100.0%; Score 75; DB 3; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LPHAILRLDLAGRL 15
      |||||
Db      46 LPHAILRLDLAGRL 60

RESULT 13
AAG26467
ID AAG26467 standard; protein; 135 AA.
XX
AC AAG26467;
DT 17-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 30933.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
FN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
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PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.

108-JUN-1999; 99US-0138094P.
10-JUN-1999; 99US-0138540P.
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21-JUL-1999; 99US-0145086P.
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22-JUL-1999; 99US-0145085P.
22-JUL-1999; 99US-0145087P.
22-JUL-1999; 99US-0145089P.
22-JUL-1999; 99US-0145192P.
23-JUL-1999; 99US-0145145P.
23-JUL-1999; 99US-0145218P.
23-JUL-1999; 99US-0145224P.
26-JUL-1999; 99US-0145276P.
27-JUL-1999; 99US-0145913P.
27-JUL-1999; 99US-0145918P.
27-JUL-1999; 99US-0145919P.
28-JUL-1999; 99US-0145951P.
02-AUG-1999; 99US-0146386P.
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03-AUG-1999; 99US-0147038P.
04-AUG-1999; 99US-0147204P.
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06-AUG-1999; 99US-0147303P.
06-AUG-1999; 99US-0147416P.
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PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148311P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
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PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
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PR 25-AUG-1999; 99US-0150566P.
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PR 27-AUG-1999; 99US-0151080P.
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PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
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PR 20-SEP-1999; 99US-0154779P.
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PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
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PR 06-OCT-1999; 99US-0157865P.
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PR 12-OCT-1999; 99US-0158369P.
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PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
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PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 100.0%; Score 75; DB 3; Length 135;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPFAILRLDLAARDL 15
Db 63 LPFAILRLDLAARDL 77

RESULT 14

ADK36534
ID ADK36534 standard; protein; 148 AA.

XX ADK36534;

XX 06-MAY-2004 (first entry)

DE Novel human polypeptide SeqID8616.

XX antiarthritic; antiparkinsonian; neuroprotective; nootropic;
KW immunosuppressive; cytostatic; antiparasitic; antiinflammatory;
KW antibacterial; antiviral; antifungal; antiparasitic; gene therapy;
KW arthritis; Parkinson's; Alzheimer's; autoimmune disease; cancer;
KW psoriasis; inflammatory bowel disease; infection; bacteria; virus;
KW fungus; parasite; human.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 1..148

FT /label= OTHER

FT /note= "OTHER= All Xaa's in this sequence are unknown
amino acids or the site of a stop codon within the DNA
sequence"

XX WO200216439-A2.

XX 28-FEB-2002.

XX 05-MAR-2001; 2001WO-US004941.

XX 07-MAR-2000; 2000US-00519705.

XX 19-MAY-2000; 2000US-00574454.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2002-280918/32.

XX Isolated polynucleotide encoding bone marrow derived polypeptides useful
for treating, e.g., Parkinson's, Alzheimer's, cancer, arthritis, Crohn's
disease, and inflammatory bowel disease.

XX Claim 20; SEQ ID NO 8616; 504pp; English.

XX This invention relates to a novel isolated polynucleotide comprising a
nucleotide sequence selected from one of 1680 sequences, a mature protein
coding portion of them, an active domain of them and their complementary
sequences. The invention may be useful for the production of compounds
with an antiarthritic, antiparkinsonian, neuroprotective, nootropic,
immunosuppressive, cytostatic, antiparasitic, antiinflammatory,
antibacterial, antiviral, antifungal or antiparasitic activity. In
addition, the disclosed sequences may be useful for gene therapy. The
polypeptides or their antibodies are useful for treating many diseases
such as arthritis, Parkinson's, Alzheimer's, autoimmune diseases, cancer,
psoriasis, inflammatory bowel disease and infections caused by bacteria,
viruses, fungi or parasites. The present sequence is that of a human
polypeptide of the invention.

SQ Sequence 148 AA;

Query Match 100.0%; Score 75; DB 5; Length 148;

Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPFAILRLDLAARDL 15

Search completed: April 8, 2005, 10:50:46
Job time : 63.4 secs

30 LPHALLRLDLGRDL 44

RESULT 15

ABG15101
ID ABG15101 standard; protein; 150 AA.

XX AC ABG15101;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #15092.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI: 2001-639362/73.

XX DR N-PSDB; AAS79288.

PT New isolated polynucleotide and encoded polypeptides, useful in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits and to assess
biodiversity.

XX PS Claim 20; SEQ ID NO 45460; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
sequences. (I) is useful as hybridisation probes, polymerase chain
reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
and in recombinant production of (II). The polynucleotides are also used
in diagnostics as expressed sequence tags for identifying expressed
genes. (I) is useful in gene therapy techniques to restore normal
activity of (II) or to treat disease states involving (II). (II) is
useful for generating antibodies against it, detecting or quantitating a
polypeptide in tissue, as molecular weight markers and as a food
supplement. (II) and its binding partners are useful in medical imaging
of sites expressing (II). (I) and (II) are useful for treating disorders
involving aberrant protein expression or biological activity. The
polypeptide and polynucleotide sequences have applications in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits to assess biodiversity
and to produce other types of data and products dependent on DNA and
amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
amino acid sequences of the invention. Note: the sequence data for this
patent did not appear in the printed specification, but was obtained in
electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 150 AA;

Query Match 100.0%; Score 75; DB 4; Length 150;

Best Local Similarity 100.0%; Pred. No. 3.6e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPHALLRLDLGRDL 15

DB 133 LPHALLRLDLGRDL 147

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:57 ; Search time 17.5333 Seconds
(without alignments)
63.863 Million cell updates/sec

Title: US-09-423-351C-7
Perfect score: 75
Sequence: 1 LPHAILRLDLGRDL 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	100.0	146	3 US-09-306-446C-5	Sequence 5, Appli
2	75	100.0	374	3 US-08-609-236-6	Sequence 6, Appli
3	75	100.0	374	3 US-09-306-446C-2	Sequence 2, Appli
4	75	100.0	375	2 US-08-494-151-14	Sequence 14, Appl
5	75	100.0	375	4 US-09-976-594-731	Sequence 731, Appl
6	75	100.0	399	4 US-09-949-016-9424	Sequence 9424, Ap
7	75	100.0	404	4 US-09-949-016-11313	Sequence 11313, A
8	73	97.3	239	4 US-09-949-016-10409	Sequence 10409, A
9	73	97.3	375	3 US-09-106-217-16	Sequence 16, Appl
10	73	97.3	376	1 US-08-588-113-2	Sequence 2, Appli
11	73	97.3	376	4 US-09-949-016-6100	Sequence 6100, Ap
12	73	97.3	377	3 US-09-106-217-2	Sequence 2, Appli
13	73	97.3	377	4 US-09-917-254-53	Sequence 53, Appl
14	73	97.3	386	4 US-09-949-016-7721	Sequence 7721, Ap
15	73	97.3	402	4 US-09-949-016-10757	Sequence 10757, A
16	69	92.0	377	4 US-09-248-796A-14109	Sequence 14109, A
17	65	86.7	375	3 US-09-171-337A-8	Sequence 8, Appli
18	65	86.7	375	4 US-09-631-022-8	Sequence 8, Appli
19	64	85.3	375	3 US-09-171-337A-7	Sequence 7, Appli
20	64	85.3	375	4 US-09-631-022-7	Sequence 7, Appli
21	64	85.3	377	4 US-09-919-172-33	Sequence 33, Appl
22	61	81.3	362	4 US-09-949-016-7725	Sequence 7725, Ap
23	61	81.3	371	1 US-08-261-208A-77	Sequence 77, Appl
24	61	81.3	376	4 US-09-538-092-1109	Sequence 1109, Ap
25	60	80.0	376	4 US-09-538-092-1110	Sequence 1110, Ap
26	60	80.0	376	4 US-09-949-016-6656	Sequence 6656, Ap
27	60	80.0	376	4 US-09-949-016-8452	Sequence 8452, Ap

28	55	73.3	394	4	US-09-949-016-6655	Sequence 6655, Ap
29	55	73.3	406	4	US-09-949-016-7396	Sequence 7396, Ap
30	55	66.7	336	4	US-09-248-796A-14108	Sequence 14108, A
31	46	61.3	670	4	US-09-252-991A-22079	Sequence 22079, A
32	45	60.0	327	4	US-09-252-991A-29837	Sequence 29837, A
33	42	56.0	1056	4	US-09-252-991A-24162	Sequence 24162, A
34	41	54.7	176	4	US-09-902-540-13432	Sequence 13432, A
35	41	54.7	354	4	US-09-252-991A-18669	Sequence 18669, A
36	41	54.7	384	4	US-09-538-092-395	Sequence 395, App
37	41	54.7	925	4	US-09-252-991A-20697	Sequence 20697, A
38	41	54.7	1121	4	US-08-915-048A-2	Sequence 2, Appli
39	40	53.3	550	4	US-09-252-991A-21032	Sequence 21032, A
40	40	53.3	917	4	US-09-902-540-12845	Sequence 12845, A
41	40	53.3	1180	4	US-09-252-991A-32464	Sequence 32464, A
42	39	52.0	182	4	US-09-583-110-4365	Sequence 4365, Ap
43	39	52.0	187	4	US-09-107-433-2893	Sequence 2893, Ap
44	39	52.0	271	4	US-09-252-991A-30514	Sequence 30514, A
45	39	52.0	425	3	US-09-036-315-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-306-446C-5
; Sequence 5, Application US/09306446C
; Patent No. 6372959
; GENERAL INFORMATION:
; APPLICANT: KIM, Dong Soo
; APPLICANT: KIM, Chul Geun
; APPLICANT: NAM, Yoon Kwon
; APPLICANT: NOH, Jae Koo
; APPLICANT: CHO, Kyoun Nam
; TITLE OF INVENTION: EXPRESSION VECTOR OF MUD LOACH GROWTH HORMONE GENE
; FILE REFERENCE: P06344US0/BAS
; CURRENT APPLICATION NUMBER: US/09306,446C
; CURRENT FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: KR 98/20255
; PRIOR FILING DATE: 1998-06-01
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Misgurnus mizolepus
US-09-306-446C-5

Query Match 100.0%; Score 75; DB 3; Length 146;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPHAILRLDLGRDL 15
DB 50 LPHAILRLDLGRDL 64

RESULT 2
US-08-609-236-6
; Sequence 6, Application US/08609236
; Patent No. 6087398
; GENERAL INFORMATION:
; APPLICANT: Steven R. Goodman
; TITLE OF INVENTION: No. 6087398el Sickle Cell Anemia Treatment
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McGregor & Adler, LLP
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

;; COMPUTER: Apple Macintosh
;; OPERATING SYSTEM: Macintosh
;; SOFTWARE: Microsoft Word for Macintosh
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/609,236
;; FILING DATE: March 1, 1996
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/002,288
;; FILING DATE: August 14, 1995
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Benjamin Aaron Adler, Ph.D.
;; REGISTRATION NUMBER: 35,423
;; REFERENCE/DOCKET NUMBER: D5807
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 713-777-2321
;; TELEFAX: 713-777-6908
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 374
;; TYPE: Amino acid
;; STRANDEDNESS:
;; TOPOLOGY: Linear
;; MOLECULE TYPE: Protein
;; DESCRIPTION: Protein
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE:
;; ORIGINAL SOURCE:
;; STRAIN:
;; INDIVIDUAL ISOLATE:
;; DEVELOPMENTAL STAGE:
;; TISSUE TYPE:
;; CELL TYPE:
;; CELL LINE:
US-08-609-236-6

Query Match 100.0%; Score 75; DB 3; Length 374;
Best Local Similarity 100.0%; Pred. No. 7.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLGRDL 15
Db 170 LPHAILRLDLGRDL 184

RESULT 3
US-09-306-446C-2
; Sequence 2, Application US/09306446C
; Patent No. 6372959
; GENERAL INFORMATION:
; APPLICANT: KIM, Dong Soo
; APPLICANT: KIM, Chul Geun
; APPLICANT: NAM, Yoon Kwon
; APPLICANT: NOH, Jae Koo
; APPLICANT: CHO, Kyou Nam
; TITLE OF INVENTION: EXPRESSION VECTOR OF MUD LOACH GROWTH HORMONE GENE
; FILE REFERENCE: P06344US0/BAS
; CURRENT APPLICATION NUMBER: US/09/306,446C
; CURRENT FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: KR 98/20255
; PRIOR FILING DATE: 1998-06-01
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Misgurnus mizolepus
US-09-306-446C-2

Query Match 100.0%; Score 75; DB 3; Length 374;
Best Local Similarity 100.0%; Pred. No. 7.7e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LPHAILRLDLGRDL 15
Db 171 LPHAILRLDLGRDL 185

RESULT 4
US-08-494-151-14
; Sequence 14, Application US/08494151
; Patent No. 5840528
; GENERAL INFORMATION:
; APPLICANT: Van Ooyen, Albert Johannes Joseph
; TITLE OF INVENTION: Transformation of Phaffia rhodozyma
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/494,151
; APPLICATION NUMBER: US/08/494,151
; FILING DATE: 23-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20039.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-494-151-14

Query Match 100.0%; Score 75; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 7.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLGRDL 15
Db 171 LPHAILRLDLGRDL 185

RESULT 5
US-09-976-594-731
; Sequence 731, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 731
; LENGTH: 375
; TYPE: PRT

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1837317CD1
US-09-976-594-731

Query Match 100.0%; Score 75; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 7.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLGRDL 15
| | | | | | | | | | | | | | | | | | | | |
Db 171 LPHAILRLDLGRDL 185

RESULT 6
US-09-949-016-9424
; Sequence 9424, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9424
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9424

Query Match 100.0%; Score 75; DB 4; Length 399;
Best Local Similarity 100.0%; Pred. No. 8.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLGRDL 15
| | | | | | | | | | | | | | | | | | | | |
Db 195 LPHAILRLDLGRDL 209

RESULT 7
US-09-949-016-11313
; Sequence 11313, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11313
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11313

Query Match 100.0%; Score 75; DB 4; Length 404;
Best Local Similarity 100.0%; Pred. No. 8.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLGRDL 15
| | | | | | | | | | | | | | | | | | | | |
Db 200 LPHAILRLDLGRDL 214

RESULT 8
US-09-949-016-10409
; Sequence 10409, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10409
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10409

Query Match 97.3%; Score 73; DB 4; Length 239;
Best Local Similarity 93.3%; Pred. No. 1.1e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLGRDL 15
| | | | | | | | | | | | | | | | | | | | |
Db 35 LPHAILRLDLGRDL 49

RESULT 9
US-09-106-217-16
; Sequence 16, Application US/09106217
; Patent No. 6063576
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Olson, Timothy M.
; TITLE OF INVENTION: Actin Mutations in Dilated
; TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; STREET: Tower
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,217
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.

REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 2323-125
TELEPHONE: 202-783-6040
TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-106-217-16

Query Match 97.3%; Score 73; DB 3; Length 375;
Best Local Similarity 93.3%; Pred. No. 1.8e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLGRDL 15
||||:|||||
Db 171 LPHAIMRLDLGRDL 185

RESULT 10

US-08-588-113-2
Sequence 2, Application US/08588113
Patent No. 5710003
GENERAL INFORMATION:
APPLICANT: McHugh, Kirk M.
TITLE OF INVENTION: DIAGNOSTIC TEST FOR DETERMINING
MALIGNANCY OF SMOOTH MUSCLE TUMORS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No 571003ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,113
FILING DATE:

CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Ralph, Rebecca L.
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: TJU-1652
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-588-113-2

Query Match 97.3%; Score 73; DB 1; Length 376;
Best Local Similarity 93.3%; Pred. No. 1.8e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLGRDL 15
||||:|||||
Db 172 LPHAIMRLDLGRDL 186

RESULT 11

US-09-949-016-6100
Sequence 6100, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6100
LENGTH: 376
TYPE: PRT
ORGANISM: Human
US-09-949-016-6100

Query Match 97.3%; Score 73; DB 4; Length 376;
Best Local Similarity 93.3%; Pred. No. 1.8e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLGRDL 15
||||:|||||
Db 172 LPHAIMRLDLGRDL 186

RESULT 12

US-09-106-217-2
Sequence 2, Application US/09106217
Patent No. 6063576
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Olson, Timothy M.
TITLE OF INVENTION: Actin Mutations in Dilated
Cardiomyopathy, a Heritable Form of Heart Failure
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rotwell, Figg, Ernst & Kurz, P.C.
STREET: 555 Thirteenth Street, N.W., Suite 701 East
STREET: Tower
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,217
FILING DATE:

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 2323-125
TELEPHONE: 202-783-6040
TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 377 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-106-217-2

Query Match 97.3%; Score 73; DB 3; Length 377;
Best Local Similarity 93.3%; Pred. No. 1.8e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLA9016 15
Db 173 LPHAILRLDLA9016 187

RESULT 13

US-09-917-254-53
; Sequence 53, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
; APPLICANT: Mutter, George
; TITLE OF INVENTION: Prognostic Classification of Breast Cancer
; FILE REFERENCE: B0801/7224(JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/222,093
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 53
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-917-254-53

Query Match 97.3%; Score 73; DB 4; Length 377;
Best Local Similarity 93.3%; Pred. No. 1.8e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLA9016 15
Db 173 LPHAILRLDLA9016 187

RESULT 14

US-09-949-016-7721
; Sequence 7721, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7721
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7721

Query Match 97.3%; Score 73; DB 4; Length 386;
Best Local Similarity 93.3%; Pred. No. 1.9e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLA9016 15
Db 182 LPHAILRLDLA9016 196

RESULT 15

US-09-949-016-10757
; Sequence 10757, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10757
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10757

Query Match 97.3%; Score 73; DB 4; Length 402;
Best Local Similarity 93.3%; Pred. No. 2e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLA9016 15
Db 198 LPHAILRLDLA9016 212

Search completed: April 8, 2005, 12:07:36
Job time : 17.5333 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 8, 2005, 10:53:18 ; Search time 42.6667 Seconds
(without alignments)
116.718 Million cell updates/sec

Title: US-09-423-351C-7

Perfect score: 75

Sequence: 1 LPHAILRLDLGRDL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 33197259 residues

Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	100.0	44	15	US-10-424-599-214884
2	75	100.0	97	9	US-09-864-761-33414
3	75	100.0	156	15	US-10-424-599-175571
4	75	100.0	168	15	US-10-264-049-4044
5	75	100.0	180	16	US-10-437-963-169247
6	75	100.0	219	14	US-10-002-631C-56
7	75	100.0	230	16	US-10-767-701-42770
8	75	100.0	236	15	US-10-424-599-206389
9	75	100.0	238	16	US-10-437-963-162706
10	75	100.0	249	16	US-10-767-701-43575
11	75	100.0	250	15	US-10-425-114-44494
12	75	100.0	254	15	US-10-425-114-69353
13	75	100.0	261	15	US-10-424-599-177530

14	75	100.0	276	15	US-10-425-114-52089	Sequence 52089, A
15	75	100.0	288	15	US-10-425-114-57500	Sequence 57500, A
16	75	100.0	299	15	US-10-424-599-278431	Sequence 278431, A
17	75	100.0	313	15	US-10-425-114-62158	Sequence 62158, A
18	75	100.0	331	15	US-10-425-114-59172	Sequence 59172, A
19	75	100.0	347	15	US-10-424-599-283333	Sequence 283333, A
20	75	100.0	371	16	US-10-322-281-68	Sequence 68, Appl
21	75	100.0	375	14	US-10-205-194-93	Sequence 93, Appl
22	75	100.0	375	14	US-10-316-253-88	Sequence 88, Appl
23	75	100.0	375	15	US-10-205-331-94	Sequence 94, Appl
24	75	100.0	375	15	US-10-260-708-82	Sequence 82, Appl
25	75	100.0	376	16	US-10-437-963-179917	Sequence 179917, A
26	75	100.0	376	16	US-10-437-963-202420	Sequence 202420, A
27	75	100.0	376	16	US-10-767-701-45677	Sequence 45677, A
28	75	100.0	376	16	US-10-767-701-46090	Sequence 46090, A
29	75	100.0	377	14	US-10-338-777-52	Sequence 52, Appl
30	75	100.0	377	15	US-10-424-599-162009	Sequence 162009, A
31	75	100.0	377	15	US-10-424-599-162685	Sequence 162685, A
32	75	100.0	377	15	US-10-424-599-162686	Sequence 162686, A
33	75	100.0	377	15	US-10-424-599-222816	Sequence 222816, A
34	75	100.0	377	15	US-10-424-599-223492	Sequence 223492, A
35	75	100.0	377	15	US-10-424-599-283336	Sequence 283336, A
36	75	100.0	377	15	US-10-425-114-66124	Sequence 66124, A
37	75	100.0	377	16	US-10-437-963-121952	Sequence 121952, A
38	75	100.0	377	16	US-10-437-963-148877	Sequence 148877, A
39	75	100.0	377	16	US-10-437-963-198295	Sequence 198295, A
40	75	100.0	377	16	US-10-767-701-47239	Sequence 47239, A
41	75	100.0	378	15	US-10-425-114-36824	Sequence 36824, A
42	75	100.0	378	15	US-10-425-114-42317	Sequence 42317, A
43	75	100.0	378	15	US-10-425-114-52458	Sequence 52458, A
44	75	100.0	378	15	US-10-425-114-59265	Sequence 59265, A
45	75	100.0	378	15	US-10-425-114-59967	Sequence 59967, A

ALIGNMENTS

RESULT 1

US-10-424-599-214884

; Sequence 214884, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 214884

; LENGTH: 44

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_36066C.1.pep

US-10-424-599-214884

Query Match 100.0%; Score 75; DB 15; Length 44;

Best Local Similarity 100.0%; Pred. No. 8.8e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLGRDL 15

Db 27 LPHAILRLDLGRDL 41

RESULT 2

US-09-864-761-33414

; Sequence 33414, Application US/09864761

; Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
SEQ ID NO 33414
LENGTH: 97
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC006483.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 18
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 48
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 81
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 28
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 85
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 78
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 37
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 45
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 40
OTHER INFORMATION: EST HUMAN HIT: BE271730.1, EVALUATE 3.00e-50
OTHER INFORMATION: SWISSPROT HIT: O42161, EVALUATE 4.00e-51
OTHER INFORMATION: EST_HUMAN HIT: BE256272.1, EVALUATE 4.00e-50

US-09-864-761-33414

Query Match 100.0%; Score 75; DB 9; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLGRDL 15
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Db 50 LPHAILRLDLGRDL 64
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RESULT 3

US-10-424-599-175571
Sequence 175571, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 175571
LENGTH: 156
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_129559C.1.pap
US-10-424-599-175571

Query Match 100.0%; Score 75; DB 15; Length 156;
Best Local Similarity 100.0%; Pred. No. 3.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLGRDL 15
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Db 34 LPHAILRLDLGRDL 48
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RESULT 4

US-10-264-049-4044
Sequence 4044, Application US/10264049
Publication No. US20040005579A1
GENERAL INFORMATION:
APPLICANT: Birse et al.
FILE REFERENCE: PA133P1
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: US 60/209,467
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 4044
LENGTH: 168
TYPE: PRT
ORGANISM: Homo sapiens
US-10-264-049-4044

Query Match 100.0%; Score 75; DB 15; Length 168;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLGRDL 15
|||||
Db 57 LPHAILRLDLGRDL 71
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RESULT 5

US-10-437-963-169247
Sequence 169247, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:

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; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 169247
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_67685C.1.pep
US-10-437-963-169247

Query Match      100.0%; Score 75; DB 16; Length 180;
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LPHAILRLDLAGRDL 15
Db      106 LPHAILRLDLAGRDL 120

RESULT 6
US-10-002-631C-56
; Sequence 56, Application US/10002631C
; Publication No. US20030157486A1
; GENERAL INFORMATION:
; APPLICANT: Graff, Jonathon M.
; APPLICANT: Muenster, Matthew
; TITLE OF INVENTION: METHODS TO IDENTIFY SIGNAL SEQUENCES
; FILE REFERENCE: A34943 090495.0243
; CURRENT APPLICATION NUMBER: US/10/002,631C
; CURRENT FILING DATE: 2001-10-31
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/300,309
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-631C-56

Query Match      100.0%; Score 75; DB 14; Length 219;
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LPHAILRLDLAGRDL 15
Db      198 LPHAILRLDLAGRDL 212

RESULT 7
US-10-767-701-42770
; Sequence 42770, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/767,701
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; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 42770
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C17410_1.pep
US-10-767-701-42770

Query Match      100.0%; Score 75; DB 16; Length 230;
Best Local Similarity 100.0%; Pred. No. 5.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LPHAILRLDLAGRDL 15
Db      173 LPHAILRLDLAGRDL 187

RESULT 8
US-10-424-599-206389
; Sequence 206389, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 206389
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(236)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_28396C.1.pep
US-10-424-599-206389

Query Match      100.0%; Score 75; DB 15; Length 236;
Best Local Similarity 100.0%; Pred. No. 5.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LPHAILRLDLAGRDL 15
Db      41 LPHAILRLDLAGRDL 55

RESULT 9
US-10-437-963-162706
; Sequence 162706, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
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; SEQ ID NO 177530
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_131325C.1.pep
US-10-424-599-177530

Query Match      100.0%;   Score 75;   DB 15;   Length 261;
Best Local Similarity 100.0%;   Pred. No. 6.2e-05;

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Job time : 42.6667 secs

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Qy 1 LPHAILRLDLAAGRL 15
Db 57 LPHAILRLDLAAGRL 71

RESULT 14
US-10-425-114-52089
; Sequence 52089, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 52089
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701149157_FLI.pap
US-10-425-114-52089

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Qy 1 LPHAILRLDLAAGRL 15
Db 72 LPHAILRLDLAAGRL 86

RESULT 15
US-10-425-114-57500
; Sequence 57500, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 57500
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMROB73004G09_FLI.pap
US-10-425-114-57500

Query Match 100.0%; Score 75; DB 15; Length 288;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLAAGRL 15
Db 84 LPHAILRLDLAAGRL 98

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 09:58:56 ; Search time 9.33333 Seconds
(without alignments)
154.634 Million cell updates/sec

Title: US-09-423-351C-7

Perfect score: 75

Sequence: 1 LPHAILRLDLAGRDL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	100.0	92	A31409	actin - California
2	75	100.0	195	S20097	actin 85c - potato
3	75	100.0	325	JC2008	actin homolog prot
4	75	100.0	327	S11452	actin (clone 302)
5	75	100.0	328	S05430	actin beta - grass
6	75	100.0	361	S68089	actin 2 - Arabidop
7	75	100.0	362	A26559	actin type 5, cyto
8	75	100.0	362	S68090	actin 8 - Arabidop
9	75	100.0	370	A29664	actin - sea urchin
10	75	100.0	374	ATBOB	actin beta - bovin
11	75	100.0	374	ATBOG	actin gamma - bovi
12	75	100.0	374	JC5818	gamma-actin - huma
13	75	100.0	375	ATKIC	actin beta - rat
14	75	100.0	375	1 A48324	actin beta, cytosk
15	75	100.0	375	1 ATAX	actin - Acanthamo
16	75	100.0	375	1 ATCHB	actin beta - chick
17	75	100.0	375	1 ATDO	actin - slime mold
18	75	100.0	375	1 ATHUB	actin beta - human
19	75	100.0	375	1 ATHSG	actin gamma 1 - hu
20	75	100.0	375	1 ATMSB	actin beta - mouse
21	75	100.0	375	1 ATMSG	actin gamma - mous
22	75	100.0	375	1 ATRRB	actin beta, non-mu
23	75	100.0	375	1 ATZM1	actin - maize
24	75	100.0	375	1 S11222	actin gamma, cytos
25	75	100.0	375	2 S71125	actin beta-2, cyto
26	75	100.0	375	2 S71124	actin beta-1, cyto
27	75	100.0	375	2 S71126	actin beta, cyto
28	75	100.0	375	2 A55001	actin beta - goose
29	75	100.0	375	2 S42103	actin - Puccinia 9

30	75	100.0	375	2	S70377	actin - Phaffia rh
31	75	100.0	376	1	ATFF7	actin 7 - fruit fl
32	75	100.0	376	1	ATSY3	actin - soybean
33	75	100.0	376	1	A43552	actin gamma, cytos
34	75	100.0	376	1	ATAXE	actin - Entamoeba
35	75	100.0	376	1	ATFF8	actin 8 - fruit fl
36	75	100.0	376	1	ATFFY	actin - slime mold
37	75	100.0	376	1	ATRZ3	actin 3 - rice
38	75	100.0	376	1	ATURS	actin Cy1 - sea ur
39	75	100.0	376	2	B23412	actin 12 - slime m
40	75	100.0	376	2	A48449	Actin-1A - nematod
41	75	100.0	376	2	S04538	actin 87E - fruit
42	75	100.0	376	2	JC1246	actin - fruit fly
43	75	100.0	376	2	JS0189	actin, cytosolic -
44	75	100.0	376	2	JS0190	actin, muscle - st
45	75	100.0	376	2	S07288	actin 15A - sea ur

ALIGNMENTS

RESULT 1

A31409 actin - California sea hare (fragments)
C:Species: Aplysia californica (California sea hare)
C>Date: 31-Mar-1990 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C:Accession: A31409; A60977
R:Kennedy, T.E.; Gawinowicz, M.A.; Barzilai, A.; Kandel, E.R.; Sweatt, J.D.
Proc. Natl. Acad. Sci. U.S.A. 85, 7008-7012, 1988
A:Title: Sequencing of proteins from two-dimensional gels by using in situ digestion and
tion in Aplysia.
A:Reference number: A94207; MUID:88320566; PMID:3413132
A:Accession: A31409
A:Molecule type: protein
A:Residues: 1-18;21-92 <KEN>
A:Cross-references: UNIPROT:Q7M3Y5
R:Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawinowicz, M.A.; Barzilai, A.; Karl, K.
Electrophoresis 10, 152-157, 1989
A:Title: Development of a database of amino acid sequences for proteins identified and
A:Reference number: A60977; MUID:89276264; PMID:2731514
A:Accession: A60977
A:Molecule type: protein
A:Residues: 1-20 <SWE>
C:Superfamily: actin

Query Match 100.0%; Score 75; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 9.5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLAGRDL 15

Db 41 LPHAILRLDLAGRDL 55

RESULT 2

S20097 actin 85c - potato (fragment)
C:Species: Solanum tuberosum (potato)
C>Date: 22-Nov-1993 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004
C:Accession: S20097
R:Drouin, G.; Dover, G.A.
J. Mol. Evol. 31, 132-150, 1990
A:Title: Independent gene evolution in the potato actin gene family demonstrated by phy
A:Reference number: S20092; MUID:91012599; PMID:2120451
A:Accession: S20097
A:Molecule type: DNA
A:Residues: 1-195 <DRO>
A:Cross-references: UNIPROT:P30170; EMBL:X55747; NID:G21541; PIDN:CAA39277.1; PID:G13455
C:Genetics:
A:Introns: 132/1
C:Superfamily: actin
C:Keywords: cytoskeleton; structural protein


```
RESULT 8
S68090
actin 8 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 05-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S68090
R:McDowell, J.M.; Huang, S.; McKinney, E.C.; An, Y.Q.; Meagher, R.B.
Genetics 142, 587-602, 1996
A>Title: Structure and evolution of the actin gene family in Arabidopsis thaliana.
A:Reference number: S68089; MUID:96158109; PMID:8852856
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-362 <MCD>
A:Cross-references: UNIPROT:O8L894
A:Note: mRNA sequencing was also done
C:Genetics:
A:Gene: ACT8
C:Superfamily: actin
C:Keywords: Cytoskeleton; structural protein

Query Match 100.0%; Score 75; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLGRDL 15
Db 165 LPHAILRLDLGRDL 179

RESULT 9
A29664
actin - sea urchin (Strongylocentrotus purpuratus)
C:Species: Strongylocentrotus purpuratus (purple urchin)
C>Date: 15-Dec-1988 #sequence_revision 30-Sep-1991 #text_change 05-Dec-1997
C:Accession: A29664
R:Crain Jr., W.R.; Boshar, M.F.; Cooper, A.D.; Durica, D.S.; Nagy, A.; Steffen, D.
J. Mol. Evol. 25, 37-45, 1987
A>Title: The sequence of a sea urchin muscle actin gene suggests a gene conversion with
A:Reference number: A29664; MUID:87311761; PMID:3114500
A:Accession: A29664
A:Molecule type: DNA
A:Residues: 1-370 <CRA>
A:Cross-references: GB:X05739; GB:X05740; GB:X05741; GB:X05742; GB:X05743
A:Note: the authors translated the codon CAG for residue 260 as Glu
C:Superfamily: actin
C:Keywords: methylated amino acid
P,73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 75; DB 2; Length 370;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLGRDL 15
Db 168 LPHAILRLDLGRDL 182

RESULT 10
ATBOB
actin beta - bovine (tentative sequence)
C:Species: Bos primigenius taurus (cattle)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: E14185; A39105; A02999; A14185
R:Vandekerckhove, J.; Weber, K.
Eur. J. Biochem. 90, 451-462, 1978
A>Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain
A:Reference number: A14185; MUID:79045349; PMID:213279
A:Accession: E14185
A:Molecule type: protein
A:Residues: 1-374 <VAN>

A:Cross-references: UNIPROT:P60712
A:Note: only peptides that differed in composition from the corresponding peptides of ra
R:Degen, J.L.; Neubauer, M.G.; Degen, S.J.F.; Seyfried, C.E.; Morris, D.R.
J. Biol. Chem. 258, 12153-12162, 1983
A>Title: Regulation of protein synthesis in mitogen-activated bovine lymphocytes. Analys
A:Reference number: A39105; MUID:84032385; PMID:6195151
A:Accession: A39105
A:Molecule type: mRNA
A:Residues: 76-227;344-374 <DEG>
A:Cross-references: GB:K00622; GB:K00623
A:Note: actins beta and gamma were not distinguished in this study
C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
C:Superfamily: actin
C:Keywords: blocked amino end; cell motility; cytoskeleton; methylated amino acid; micro
P,1/Modified site: blocked amino end (Asp) (probably acetylated) #status experimental
P,72/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 75; DB 1; Length 374;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLGRDL 15
Db 170 LPHAILRLDLGRDL 184

RESULT 11
ATBOG
actin gamma - bovine (tentative sequence)
C:Species: Bos primigenius taurus (cattle)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: E14185; A02999
R:Vandekerckhove, J.; Weber, K.
Eur. J. Biochem. 90, 451-462, 1978
A>Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain
A:Reference number: A14185; MUID:79045349; PMID:213279
A:Accession: E14185
A:Molecule type: protein
A:Residues: 1-374 <VAN>
A:Cross-references: UNIPROT:P02571
A:Note: only peptides that differed in composition from the corresponding peptides of ra
C:Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
C:Superfamily: actin
C:Keywords: blocked amino end; cell motility; cytoskeleton; methylated amino acid; micro
P,1/Modified site: blocked amino end (Glu) (probably acetylated) #status experimental
P,72/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 75; DB 1; Length 374;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLGRDL 15
Db 170 LPHAILRLDLGRDL 184

RESULT 12
JCS818
gamma-actin - human
C:Species: Homo sapiens (man)
C>Date: 20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C:Accession: JCS818; PC4501
R:Hauschildt, S.; Schwarz, C.; Heine, H.; Ulmer, H.J.; Flad, H.D.; Rietschel, E.T.; Jens
Biochem. Biophys. Res. Commun. 241, 670-674, 1997
A>Title: Actin: A target of lipopolysaccharide-induced phosphorylation in human monocytes
A:Reference number: JCS818; MUID:98096379; PMID:9434766
A:Accession: JCS818
A:Molecule type: protein
A:Residues: 1-374 <HAU>
A:Cross-references: UNIPROT:P02571
A:Experimental source: monocyte
A:Accession: PC4501
A:Molecule type: protein
```

A;Residues: 1-61;84-112;147-190;196-209;215-253;335-358 <HA2>

A;Experimental source: monocyte

C;Comment: This protein is involved in a signal transduction that eventually leads to m

C;Superfamily: actin

Query Match 100.0%; Score 75; DB 2; Length 374;

Best Local Similarity 100.0%; Pred. No. 4.7e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPHAILRLDLGRDL 15

Db 170 LPHAILRLDLGRDL 184

RESULT 13

ATATC

actin beta - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 22-Jun-1999

C;Accession: A38571; A02999

R;Nudel, U.; Zakut, R.; Shani, M.; Neuman, S.; Levy, Z.; Yaffe, D.

Nucleic Acids Res. 11, 1759-1771, 1983

A;Title: The nucleotide sequence of the rat cytoplasmic beta-actin gene.

A;Reference number: A38571; MUID:83168920; PMID:6300777

A;Accession: A38571

A;Molecule type: DNA

A;Residues: 1-375 <NUD>

A;Cross-references: GB:J00691; NID:G202653; PIDN:AAA40457.1; PID:G202654

C;Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,

C;Genetics:

A;Introns: 41/3; 121/3; 268/1; 328/3

C;Superfamily: actin

C;Keywords: cell motility; cytoskeleton; methylated amino acid; microfilament; mitosis;

F;2-375/Product: actin beta #status predicted <MAT>

F;73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 75; DB 1; Length 375;

Best Local Similarity 100.0%; Pred. No. 4.7e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPHAILRLDLGRDL 15

Db 171 LPHAILRLDLGRDL 185

RESULT 14

A48324

actin beta, cytoskeletal - common carp

C;Species: Cyprinus carpio (common carp)

C;Date: 03-Feb-1994 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004

C;Accession: A48324

R;Liu, Z.; Zhu, Z.; Roberg, K.; Faras, A.; Guise, K.; Kapuscinski, A.R.; Hackett, P.B.

DNA Seq. 1, 125-136, 1990

A;Title: Isolation and characterization of beta-actin gene of carp (Cyprinus carpio).

A;Reference number: A48324; MUID:92190540; PMID:2134183

A;Accession: A48324

A;Molecule type: DNA

A;Residues: 1-375 <LIU>

A;Cross-references: UNIPROT:P83750; GB:M24113; NID:G213041; PIDN:AAA68886.1; PID:G213042

A;Note: the authors translated the codon TTC for residue 21 as Pro, AAG for residue 50 a

7 as Pro

A;Note: the authors failed to translated the codon GGT for residue 42 as Gly

C;Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,

C;Genetics:

A;Introns: 41/3; 121/3; 268/3; 328/3

C;Superfamily: actin

C;Keywords: acetylated amino end; cell motility; cytoskeleton; methylated amino acid; mi

F;2-375/Product: actin beta, cytoskeletal #status predicted <MAT>

F;73/Modified site: acetylated amino end (Asp) (in mature form) #status predicted

F;73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match

Best Local Similarity 100.0%; Score 75; DB 1; Length 375;

Pred. No. 4.7e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPHAILRLDLGRDL 15

Db 171 LPHAILRLDLGRDL 185

RESULT 15

ATAX

actin - Acanthamoeba castellanii

C;Species: Acanthamoeba castellanii

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004

C;Accession: A92886; A03004

R;Nellen, W.; Gallwitz, D.

J. Mol. Biol. 159, 1-18, 1982

A;Title: Actin genes and actin messenger RNA in Acanthamoeba castellanii. Nucleotide seq

A;Reference number: A92886; MUID:83033627; PMID:6290670

A;Accession: A92886

A;Molecule type: DNA

A;Residues: 1-375 <NEL>

A;Cross-references: UNIPROT:P02578; GB:V00002; GB:J01016; NID:G5565; PIDN:CAA33399.1; PFI

C;Comment: There are at least three actin genes in A. castellanii.

C;Genetics:

A;Introns: 105/3

C;Superfamily: actin

C;Keywords: methylated amino acid

F;73/Modified site: 3'-methylhistidine (His) #status predicted

Query Match 100.0%; Score 75; DB 1; Length 375;

Best Local Similarity 100.0%; Pred. No. 4.7e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPHAILRLDLGRDL 15

Db 171 LPHAILRLDLGRDL 185

Search completed: April 8, 2005, 10:53:06

Job time : 10.3333 secs

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RP SEQUENCE.
MEDLINE=89276264; PubMed=2731514;
SWEAT J.D., Kennedy T.E., Wager-Smith K., Gawinowicz M.A.,
BARZILAI A., KARL K.A., Kandel E.R.;
"Development of a database of amino acid sequences for proteins
identified and isolated on two-dimensional polyacrylamide gels.";
Electrophoresis 10:152-157(1989).
PIR; A31409; A31409.
GO; GO:0015629; C:actin cytoskeleton; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
NON_TER 1
NON_TER 92
SEQUENCE 92 AA; 9513 MW; 3C36BEFE381A701C CRC64;

Query Match 100.0%; Score 75; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. NO. 3.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPFAILRLDLGRDL 15
|||||
41 LPFAILRLDLGRDL 55

DB

RESULT 2
Q6VQP9
Q6VQP9 PRELIMINARY; PRT; 93 AA.
AC Q6VQP9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Actin (Fragment).

```

```
OS Romalea microptera (Lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Romaleidae; Romalea.
OX NCBI_TaxID=7007;
RN [1]
RP SEQUENCE FROM N.A.
RA Fei H., Martin T., Jaskowiak K., Hatle J., Borst D.W.,
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY331667; AAQ24502.1; -.
FT NON TER 1
SQ SEQUENCE 93 AA; 10698 MW; 5635F5335A532256 CRC64;

Query Match 100.0%; Score 75; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLGRDL 15
Db 13 LPHAILRLDLGRDL 27

RESULT 3
O61569 ID O61569 PRELIMINARY; PRT; 101 AA.
AC O61569;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Actin (Fragment).
GN Name=act;
OS Ostertagia ostertagi.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC Trichostrongyloidea; Haemonchidae; Ostertagiinae; Ostertagia.
OX NCBI_TaxID=6317;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20233682; PubMed=10769181; DOI=10.1042/0264-6021:3470763;
RA Moore J., Tetley L., Devaney E.;
RT "Identification of abundant mRNAs from the third stage larvae of the
RT parasitic nematode, Ostertagia ostertagi.";
RL Biochem. J. 347:763-770(2000).
DR EMBL; AF052043; AAC06292.1; -.
DR HSSP; P10983; 1D4X.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON TER 1
FT NON TER 101
SQ SEQUENCE 101 AA; 11499 MW; 7AF3A21892AD0D75 CRC64;

Query Match 100.0%; Score 75; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 4.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLGRDL 15
Db 8 LPHAILRLDLGRDL 22

RESULT 4
Q11210 ID Q11210 PRELIMINARY; PRT; 104 AA.
AC Q11210;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta-actin (Fragment)
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
```

```
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=lung;
RA Hino A., Tokuyama Y., Kobayashi M., Yano M., Weir B., Takeda J.,
RA Bell G.I., MacDonald R.L.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U20576; AAA62435.1; -.
DR HSSP; P10983; 1D4X.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON TER 1
FT NON TER 104
SQ SEQUENCE 104 AA; 11438 MW; 3610F3FEFA370C91 CRC64;

Query Match 100.0%; Score 75; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLGRDL 15
Db 42 LPHAILRLDLGRDL 56

RESULT 5
Q28916 ID Q28916 PRELIMINARY; PRT; 109 AA.
AC Q28916;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Actin (Fragment).
OS Macaca fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9542;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96071113; PubMed=7577717; DOI=10.1016/0960-0760(95)00157-U;
RA Yamada-Mouri N., Hirata S., Hayashi M., Kato J.;
RT "Analysis of the expression and the first exon of aromatase mRNA in
RT monkey brain.";
RL J. Steroid Biochem. Mol. Biol. 55:17-23(1995).
DR EMBL; S79782; AB35618.2; -.
DR HSSP; P10983; 1D4X.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON TER 1
FT NON TER 109
SQ SEQUENCE 109 AA; 12333 MW; 64A64E108CDDA54C CRC64;

Query Match 100.0%; Score 75; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLGRDL 15
Db 56 LPHAILRLDLGRDL 70

RESULT 6
Q841A4 ID Q841A4 PRELIMINARY; PRT; 109 AA.
AC Q841A4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Actin (Fragment).
```

OS Festuca arundinacea (Tall fescue) (Schedonorus arundinaceus).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Poaceae; Schedonorus.
OX NCBI_TaxID=4606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pseudostem;
RA Johnson L.J., Johnson R.D., Schardl C.L., Panaccione D.G.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY194227; AAC04042.2; -.
DR HSSP; P02577; INMI.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 12177 MW; 10780BBAS2F6E8EA CRC64;

Query Match 100.0%; Score 75; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LPFAILRLDLGRDL 15
Db 52 LPFAILRLDLGRDL 66

RESULT 7
Q80012 PRELIMINARY; PRT; 117 AA.
AC Q80012; 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-actin 2 (Fragment).
GN Name=ACTB2;
OS Hyla japonica (Japanese tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae; Hylinae;
OC Hyla.
OX NCBI_TaxID=109175;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Kohno S., Kamishima Y., Iguchi T.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AB092519; BAC66207.1; -.
DR HSSP; P60712; 1HLU.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13291 MW; 64C6BAC4F84184CF CRC64;

Query Match 100.0%; Score 75; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LPFAILRLDLGRDL 15
Db 92 LPFAILRLDLGRDL 106

RESULT 8
Q80013 PRELIMINARY; PRT; 117 AA.
AC Q80013; 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-actin 1 (Fragment).
GN Name=ACTB1;
OS Hyla japonica (Japanese tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae; Hylinae;
OC Hyla.
OX NCBI_TaxID=109175;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Kohno S., Kamishima Y., Iguchi T.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AY227658; AAC02722.1; -.
DR HSSP; P60712; 1HLU.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.

Query Match 100.0%; Score 75; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LPFAILRLDLGRDL 15
Db 92 LPFAILRLDLGRDL 106

RESULT 9
Q802E1 PRELIMINARY; PRT; 125 AA.
AC Q802E1; 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta actin (Fragment).
GN Name=ACT-B;
OS Zoarces viviparus (Belout).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Zoarcoidei;
OC Zoarcidae; Zoarces.
OX NCBI_TaxID=48416;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Lucassen M., Sokolov E., Poertner H.-O.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AY227658; AAC02722.1; -.
DR HSSP; P60712; 1HLU.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.

```
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON_TER 1
FT NON_TER 125
SQ SEQUENCE 125 AA; 14100 MW; 7B33EA4CF5EA8B0 CRC64;

Query Match 100.0%; Score 75; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLGRDL 15
| | | | | | | | | | | | | | |
Db 85 LPHAILRLDLGRDL 99

RESULT 10
Q802E2 PRELIMINARY; PRT; 125 AA.
AC Q802E2;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Beta actin (Fragment).
CN Name=ACT-B;
OS Pachycara brachycephalum (Antarctic eelpout) (Austrolycichthys brachycephalus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Zoarcoidei;
OC Zoarcidae; Pachycara.
OX NCBI_TaxID=36221;
RN [1]
RP SEQUENCE FROM N.A.
RA Lucassen M., Sokolov E., Poertner H.-O.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AY227657; AA072721.1; -.
DR HSP; P60712; 1HLU.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005280; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON_TER 1
FT NON_TER 125
SQ SEQUENCE 125 AA; 14100 MW; 7B33EA4CF5EA8B0 CRC64;

Query Match 100.0%; Score 75; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLGRDL 15
| | | | | | | | | | | | | | |
Db 85 LPHAILRLDLGRDL 99

RESULT 11
Q852Q7 PRELIMINARY; PRT; 128 AA.
AC Q852Q7;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Actin (Fragment).
CN Name=MpAct1;
OS Marchantia polymorpha (Liverwort).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Marchantiophyta;
OC Marchantiopsida; Marchantiidae; Marchantiales; Marchantiaceae;
OC Marchantiaceae; Marchantia.
OX NCBI_TaxID=3197;
RN [1]
RP SEQUENCE FROM N.A.
RA Ahida Y., Fujii Y., Hirata T.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB100427; BAC55601.1; -.
DR HSP; P02577; 1NM1.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
FT NON_TER 1
FT NON_TER 128
SQ SEQUENCE 128 AA; 14527 MW; 53A33892EB2E608C CRC64;

Query Match 100.0%; Score 75; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLGRDL 15
| | | | | | | | | | | | | | |
Db 7 LPHAILRLDLGRDL 21

RESULT 12
Q865G0 PRELIMINARY; PRT; 130 AA.
AC Q865G0;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Beta-actin (Fragment).
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RA Sharmila C., Reddy P.G.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -!- SIMILARITY: Belongs to the actin family.
DR EMBL; AF481159; AA049278.1; -.
DR HSP; P60712; 1HLU.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON_TER 1
FT NON_TER 130
SQ SEQUENCE 130 AA; 14728 MW; E817FD365B33EA3F CRC64;

Query Match 100.0%; Score 75; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 5.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPHAILRLDLGRDL 15
| | | | | | | | | | | | | | |
Db 86 LPHAILRLDLGRDL 100

RESULT 13
Q91A84
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GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON_TER 1
FT NON_TER 133
SQ SEQUENCE 133 AA; 14955 MW; 27DFC1FF30D4984F CRC64;

Query Match 100.0%; Score 75; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 5.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPHAILRLDLGRDL 15
DB 83 LPHAILRLDLGRDL 97
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RESULT 15
QY04L8 PRELIMINARY; PRT; 133 AA.
ID ID Q9U4L8
AC Q9U4L8;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Actin 1 (Fragment).
OS Ageniaaspis citricola.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Chalcidoidea;
OC Encyrtidae; Encyrtinae; Ageniaaspis.
OX NCBI_TaxID=105762;
[1]
SEQUENCE FROM N.A.
RC STRAIN=Taiwan population;
RA Hoy M.A., Jeyaparakash A., Morakote R., Lo P.K.C., Nguyen R.;
RT "Genomic analyses of two populations of Ageniaaspis citricola
RT (Hymenoptera: Encyrtidae) suggest that a cryptic species may exist.";
RL Biol. Control 17:1-10(2000).
CC -1- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells (By similarity).
CC -1- SIMILARITY: Belongs to the actin family.
DR EMBL; AF164630; AAF22278.1; -.
DR HSSP; P10983; 1D4X.
DR GO; GO:0015629; C:actin cytoskeleton; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR004000; Actin_like.
DR Pfam; PF00022; Actin; 1.
DR PRINTS; PR00190; ACTIN.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
KW Structural protein.
FT NON_TER 1
FT NON_TER 133
SQ SEQUENCE 133 AA; 14941 MW; 62CB94BF37A39F3F CRC64;

Query Match 100.0%; Score 75; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 5.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPHAILRLDLGRDL 15
DB 83 LPHAILRLDLGRDL 97
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